#10

## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : Ashkenazi et al.

Appl. No. : 09/902,572

Filed : July 10, 2001

For : SECRETED AND TRANSMEMBRAN

POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

Examiner : Unknown

Group Art Unit Unknown

## **SEQUENCE SUBMISSION STATEMENT**

United States Patent and Trademark Office PO Box 2327 Arlington VA 22202

Dear Sir:

This is in response to the Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures, mailed May 14, 2002. I hereby state that the amendments, made in accordance with 37 C.F.R. § 1.825(a) and included in the Substitute Sequence Listing submitted herewith, are supported in the application, and that the Substitute Sequence Listing does not include new matter.

I further state that the information recorded in the currently submitted substitute copy of the computer-readable form of the Sequence Listing is identical to the paper form of the Sequence Listing submitted herewith as required in 37 C.F.R. § 1.825(b).

Please charge any additional fees, including any fees for additional extension of time, or credit overpayment to Deposit Account No. 11-1410.

Respectfully submitted,

KNOBBE, MARTENS, OLSON & BEAR, LLP

Dated: July 12, 2002

By:

Adeel S. Akhtar
Registration No. 41,394
Attorney of Record
620 Newport Center Drive, 16<sup>th</sup> Floor
Newport Beach, CA 92660
(415) 954-4114

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## SEQUENCE LISTING

<110> Generopan Ashkenazi, Avi Botstein, David Desnoyers, Luc Eaton, Dan L. Ferrara, Napoleone Filvaroff, Ellen Fong, Sherman Gao, Wei-Qiang Gerber, Hanspeter Gerritsen, Mary E. Goddard, A. Godowski, Paul J. Grimaldi, Christopher J. Gurney, Austin L. Hillan, Kenneth, J. Kljavin, Ivar J. Mather, Jennie P. Pan, James Paoni, Nicholas F. Roy, Margaret Ann Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey

Wood, William, I.

- <120> Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
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- <141> 2001-07-10
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- <150> US 60/145,698
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Thr Asp Gln Leu Ser Arg Arg Gln Ile Arg Glu Tyr Gln Leu Tyr Ser 35 40 45

Arg Thr Ser Gly Lys His Val Gln Val Thr Gly Arg Arg Ile Ser Ala
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Thr Ala Glu Asp Gly Asn Lys Phe Ala Lys Leu Ile Val Glu Thr Asp 65 70 75 80

Thr Phe Gly Ser Arg Val Arg Ile Lys Gly Ala Glu Ser Glu Lys Tyr 85 90 95

Ile Cys Met Asn Lys Arg Gly Lys Leu Ile Gly Lys Pro Ser Gly Lys
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Ser Lys Asp Cys Val Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr 115 120 125

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Gln Gly Arg Pro Arg Gln Ala Ser Arg Ser Arg Gln Asn Gln Arg Glu 145 150 155 160

Ala His Phe Ile Lys Arg Leu Tyr Gln Gly Gln Leu Pro Phe Pro Asn 165 170 175

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<213> Homo sapiens
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Cys Asn Glu Arg Ser Leu Thr Ser Val Pro Leu Gly Ile Pro Glu Gly 55

Val Thr Val Leu Tyr Leu His Asn Asn Gln Ile Asn Asn Ala Gly Phe

Pro Ala Glu Leu His Asn Val Gln Ser Val His Thr Val Tyr Leu Tyr

Gly Asn Gln Leu Asp Glu Phe Pro Met Asn Leu Pro Lys Asn Val Arg 105

Val Leu His Leu Gln Glu Asn Asn Ile Gln Thr Ile Ser Arg Ala Ala 115 120 125

Leu Ala Gln Leu Leu Lys Leu Glu Glu Leu His Leu Asp Asp Asn Ser 135 Ile Ser Thr Val Gly Val Glu Asp Gly Ala Phe Arg Glu Ala Ile Ser 150 155 Leu Lys Leu Leu Phe Leu Ser Lys Asn His Leu Ser Ser Val Pro Val 170 Gly Leu Pro Val Asp Leu Gln Glu Leu Arg Val Asp Glu Asn Arg Ile 180 Ala Val Ile Ser Asp Met Ala Phe Gln Asn Leu Thr Ser Leu Glu Arg 200 Leu Ile Val Asp Gly Asn Leu Leu Thr Asn Lys Gly Ile Ala Glu Gly 210 Thr Phe Ser His Leu Thr Lys Leu Lys Glu Phe Ser Ile Val Arg Asn Ser Leu Ser His Pro Pro Pro Asp Leu Pro Gly Thr His Leu Ile Arg 250 Leu Tyr Leu Gln Asp Asn Gln Ile Asn His Ile Pro Leu Thr Ala Phe 260 265 Ser Asn Leu Arg Lys Leu Glu Arg Leu Asp Ile Ser Asn Asn Gln Leu 280 Arg Met Leu Thr Gln Gly Val Phe Asp Asn Leu Ser Asn Leu Lys Gln 300 Leu Thr Ala Arg Asn Asn Pro Trp Phe Cys Asp Cys Ser Ile Lys Trp Val Thr Glu Trp Leu Lys Tyr Ile Pro Ser Ser Leu Asn Val Arg Gly 330 Phe Met Cys Gln Gly Pro Glu Gln Val Arg Gly Met Ala Val Arg Glu 345 Leu Asn Met Asn Leu Leu Ser Cys Pro Thr Thr Pro Gly Leu Pro 360 Leu Phe Thr Pro Ala Pro Ser Thr Ala Ser Pro Thr Thr Gln Pro Pro 370 375 Thr Leu Ser Ile Pro Asn Pro Ser Arg Ser Tyr Thr Pro Pro Thr Pro Thr Thr Ser Lys Leu Pro Thr Ile Pro Asp Trp Asp Gly Arg Glu Arg 405 410

Val Thr Pro Pro Ile Ser Glu Arg Ile Gln Leu Ser Ile His Phe Val

425

420

Asn Asp Thr Ser Ile Gln Val Ser Trp Leu Ser Leu Phe Thr Val Met 435 440 445

Ala Tyr Lys Leu Thr Trp Val Lys Met Gly His Ser Leu Val Gly Gly 450 460

Ile Val Gln Glu Arg Ile Val Ser Gly Glu Lys Gln His Leu Ser Leu 465 470 475 480

Val Asn Leu Glu Pro Arg Ser Thr Tyr Arg Ile Cys Leu Val Pro Leu 485 490 495

Asp Ala Phe Asn Tyr Arg Ala Val Glu Asp Thr Ile Cys Ser Glu Ala 500 505 510

Thr Thr His Ala Ser Tyr Leu Asn Asn Gly Ser Asn Thr Ala Ser Ser 515 520 525

His Glu Gln Thr Thr Ser His Ser Met Gly Ser Pro Phe Leu Leu Ala 530 535 540

Gly Leu Ile Gly Gly Ala Val Ile Phe Val Leu Val Val Leu Leu Ser 545 550 560

Val Phe Cys Trp His Met His Lys Lys Gly Arg Tyr Thr Ser Gln Lys 565 570 575

Trp Lys Tyr Asn Arg Gly Arg Arg Lys Asp Asp Tyr Cys Glu Ala Gly 580 585 590

Thr Lys Lys Asp Asn Ser Ile Leu Glu Met Thr Glu Thr Ser Phe Gln 595 600 605

Ile Val Ser Leu Asn Asn Asp Gln Leu Leu Lys Gly Asp Phe Arg Leu 610 615 620

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<213> Artificial Sequence

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45

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Val Asp Tyr Cys Ala Ser Glu Asn His Gly Cys Glu His Glu Cys Val

Asn Ala Asp Gly Ser Tyr Leu Cys Gln Cys His Glu Gly Phe Ala Leu

Asn Pro Asp Glu Lys Thr Cys Thr Arg Ile Asn Tyr Cys Ala Leu Asn Lys Pro Gly Cys Glu His Glu Cys Val Asn Met Glu Glu Ser Tyr Tyr Cys Arg Cys His Arg Gly Tyr Thr Leu Asp Pro Asn Gly Lys Thr Cys Ser Arg Val Asp His Cys Ala Gln Gln Asp His Gly Cys Glu Gln Leu Cys Leu Asn Thr Glu Asp Ser Phe Val Cys Gln Cys Ser Glu Gly Phe Leu Ile Asn Glu Asp Leu Lys Thr Cys Ser Arg Val Asp Tyr Cys Leu Leu Ser Asp His Gly Cys Glu Tyr Ser Cys Val Asn Met Asp Arg Ser Phe Ala Cys Gln Cys Pro Glu Gly His Val Leu Arg Ser Asp Gly Lys Thr Cys Ala Lys Leu Asp Ser Cys Ala Leu Gly Asp His Gly Cys Glu His Ser Cys Val Ser Ser Glu Asp Ser Phe Val Cys Gln Cys Phe Glu Gly Tyr Ile Leu Arg Glu Asp Gly Lys Thr Cys Arg Arg Lys Asp Val Cys Gln Ala Ile Asp His Gly Cys Glu His Ile Cys Val Asn Ser Asp Asp Ser Tyr Thr Cys Glu Cys Leu Glu Gly Phe Arg Leu Ala Glu Asp Gly Lys Arg Cys Arg Arg Lys Asp Val Cys Lys Ser Thr His His Gly Cys Glu His Ile Cys Val Asn Asn Gly Asn Ser Tyr Ile Cys Lys Cys Ser Glu Gly Phe Val Leu Ala Glu Asp Gly Arg Arg Cys Lys Lys Cys Thr Glu Gly Pro Ile Asp Leu Val Phe Val Ile Asp Gly Ser Lys Ser Leu Gly Glu Glu Asn Phe Glu Val Val Lys Gln Phe Val Thr Gly Ile Ile Asp Ser Leu Thr Ile Ser Pro Lys Ala Ala Arg Val Gly Leu Leu

Gln Tyr Ser Thr Gln Val His Thr Glu Phe Thr Leu Arg Asn Phe Asn 660 665 670

Ser Ala Lys Asp Met Lys Lys Ala Val Ala His Met Lys Tyr Met Gly 675 680 685

Lys Gly Ser Met Thr Gly Leu Ala Leu Lys His Met Phe Glu Arg Ser 690 695 700

Phe Thr Gln Gly Glu Gly Ala Arg Pro Leu Ser Thr Arg Val Pro Arg 705 710 715 720

Ala Ala Ile Val Phe Thr Asp Gly Arg Ala Gln Asp Asp Val Ser Glu 725 730 735

Trp Ala Ser Lys Ala Lys Ala Asn Gly Ile Thr Met Tyr Ala Val Gly 740 745 750

Val Gly Lys Ala Ile Glu Glu Glu Leu Gln Glu Ile Ala Ser Glu Pro 755 760 765

Thr Asn Lys His Leu Phe Tyr Ala Glu Asp Phe Ser Thr Met Asp Glu 770 780

Ile Ser Glu Lys Leu Lys Lys Gly Ile Cys Glu Ala Leu Glu Asp Ser 785 790 795 800

Asp Gly Arg Gln Asp Ser Pro Ala Gly Glu Leu Pro Lys Thr Val Gln 805 810 815

Gln Pro Thr Glu Ser Glu Pro Val Thr Ile Asn Ile Gln Asp Leu Leu 820 825 830

Ser Cys Ser Asn Phe Ala Val Gln His Arg Tyr Leu Phe Glu Glu Asp 835 840 845

Asn Leu Leu Arg Ser Thr Gln Lys Leu Ser His Ser Thr Lys Pro Ser 850 860

Gly Ser Pro Leu Glu Glu Lys His Asp Gln Cys Lys Cys Glu Asn Leu 865 870 875

Ile Met Phe Gln Asn Leu Ala Asn Glu Glu Val Arg Lys Leu Thr Gln 885 890 895

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200

205

195

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oligonucleotide probe

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Ser Gly Asn Gly Val Thr Ile Cys Glu Asp Asp Asn Glu Cys Gly Asn
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Glu Val Tyr Arg Asn Ser Val Thr Asp Leu Ser Pro Thr Asp Ile Ile
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Pro	Se:	r Il	e Gly		e Lys	s Ası	р Туз	425	ı Ile	e Lei	ı Thr	Arg	3 Ile 430	e Thi	Gln
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Ph	e Tr		e Ph	e Se	r Gl	u Il 45	e Gli 5	n Sei	r Th	r Ar	g Thi 460	Thi	r Ile	e His	s Lys
As:		u Cy	s Cy	s Se	r Le		e Le	u Ala	a Gl	u Le	u Val	L Pho	e Lei	ı Val	1 Gly 480
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485 490 495

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Leu His Lys Asn Phe Tyr Ile Phe Gly Tyr Leu Ser Pro Ala Val Val 530 540

Val Gly Phe Ser Ala Ala Leu Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys 545 550 560

Val Cys Trp Leu Ser Thr Glu Asn Asn Phe Ile Trp Ser Phe Ile Gly 565 570 575

Pro Ala Cys Leu Ile Ile Leu Val Asn Leu Leu Ala Phe Gly Val Ile 580 585 590

Ile Tyr Lys Val Phe Arg His Thr Ala Gly Leu Lys Pro Glu Val Ser 595 600 605

Cys Phe Glu Asn Ile Arg Ser Cys Ala Arg Gly Ala Leu Ala Leu Leu 610 615 620

Phe Leu Leu Gly Thr Thr Trp Ile Phe Gly Val Leu His Val Val His 625 630 635 640

Ala Ser Val Val Thr Ala Tyr Leu Phe Thr Val Ser Asn Ala Phe Gln 645 650 655

Gly Met Phe Ile Phe Leu Phe Leu Cys Val Leu Ser Arg Lys Ile Gln
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Leu Arg 690

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Thr Ser Gly Pro His Gly Leu Ser Ser Cys Phe Leu Arg Ile Arg Ala
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Ser Val Arg Tyr Leu Cys Met Gly Ala Asp Gly Lys Met Gln Gly Leu
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Pro Leu Ser His Phe Leu Pro Met Leu Pro Met Val Pro Glu Glu Pro
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Ala Cys Lys Thr Pro Lys Lys Thr Val Ser Ser Arg Leu Glu Trp Lys 50 55 60

Lys Leu Gly Arg Ser Val Ser Phe Val Tyr Tyr Gln Gln Thr Leu Gln 65 70 75 80

Gly Asp Phe Lys Asn Arg Ala Glu Met Ile Asp Phe Asn Ile Arg Ile  $85 \hspace{1cm} 90 \hspace{1cm} 95$ 

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Ala Pro Ser Glu Gln Gly Gln Asn Leu Glu Glu Asp Thr Val Thr Leu 115 120 125

Glu Val Leu Val Ala Pro Ala Val Pro Ser Cys Glu Val Pro Ser Ser 130 135 140

Ala Leu Ser Gly Thr Val Val Glu Leu Arg Cys Gln Asp Lys Glu Gly 145 150 155 160

Asn Pro Ala Pro Glu Tyr Thr Trp Phe Lys Asp Gly Ile Arg Leu Leu 165 170 175

Glu Asn Pro Arg Leu Gly Ser Gln Ser Thr Asn Ser Ser Tyr Thr Met Asn Thr Lys Thr Gly Thr Leu Gln Phe Asn Thr Val Ser Lys Leu Asp 200 Thr Gly Glu Tyr Ser Cys Glu Ala Arg Asn Ser Val Gly Tyr Arg Arg 215 Cys Pro Gly Lys Arg Met Gln Val Asp Asp Leu Asn Ile Ser Gly Ile Ile Ala Ala Val Val Val Ala Leu Val Ile Ser Val Cys Gly Leu 245 250 Gly Val Cys Tyr Ala Gln Arg Lys Gly Tyr Phe Ser Lys Glu Thr Ser 265 Phe Gln Lys Ser Asn Ser Ser Ser Lys Ala Thr Thr Met Ser Glu Asn 280 Val Gln Trp Leu Thr Pro Val Ile Pro Ala Leu Trp Lys Ala Ala Ala 295 Gly Gly Ser Arg Gly Gln Glu Phe 305 310 <210> 65 <211> 22 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 65 atcgttgtga agttagtgcc cc 22 <210> 66 <211> 23 <212> DNA <213> Artificial Sequence <223> Description of Artificial Sequence: Synthetic oligonucleotide probe <400> 66 acctgcgata tccaacagaa ttg 23 <210> 67 <211> 48 <212> DNA <213> Artificial Sequence <220>

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Glu Ala Ser Thr Val Asp Cys Asn Asp Leu Gly Leu Leu Thr Phe Pro 50 55 60

Ala Arg Leu Pro Ala Asn Thr Gln Ile Leu Leu Leu Gln Thr Asn Asn 65 70 75 80

Ile Ala Lys Ile Glu Tyr Ser Thr Asp Phe Pro Val Asn Leu Thr Gly
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Leu Asp Leu Ser Gln Asn Asn Leu Ser Ser Val Thr Asn Ile Asn Val 100 105 110

Lys Lys Met Pro Gln Leu Leu Ser Val Tyr Leu Glu Glu Asn Lys Leu 115 120 125

Thr Glu Leu Pro Glu Lys Cys Leu Ser Glu Leu Ser Asn Leu Gln Glu 130 135 140

Leu Tyr Ile Asn His Asn Leu Leu Ser Thr Ile Ser Pro Gly Ala Phe 145 150 155 160

Ile Gly Leu His Asn Leu Leu Arg Leu His Leu Asn Ser Asn Arg Leu 165 170 175

Gln Met Ile Asn Ser Lys Trp Phe Asp Ala Leu Pro Asn Leu Glu Ile 180 185 190

Leu Met Ile Gly Glu Asn Pro Ile Ile Arg Ile Lys Asp Met Asn Phe 195 200 205

Lys Pro Leu Ile Asn Leu Arg Ser Leu Val Ile Ala Gly Ile Asn Leu 210 215 220

Thr Glu Ile Pro Asp Asn Ala Leu Val Gly Leu Glu Asn Leu Glu Ser 235 230 235

Ile Ser Phe Tyr Asp Asn Arg Leu Ile Lys Val Pro His Val Ala Leu 245 250 255

Gln Lys Val Val Asn Leu Lys Phe Leu Asp Leu Asn Lys Asn Pro Ile 260 265 270

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Glu Asn Ser His Ala Ala Gln Ser Ala Arg Ile Pro Ser Asp Val Lys

570

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Leu Gly Glu Leu Tyr Pro Pro Leu Ile Asn Leu Trp Glu Ala Gly Lys
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Thr Cys Ser Asn Ala Asn Leu Lys Glu Ile Pro Arg Asp Leu Pro Pro 50 55 60

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Asn Glu Ile Phe Lys Asp Leu His Gln Leu Arg Val Leu Asn Leu Ser 85 90 95

Lys Asn Gly Ile Glu Phe Ile Asp Glu His Ala Phe Lys Gly Val Ala 100 105 110

Glu Thr Leu Gln Thr Leu Asp Leu Ser Asp Asn Arg Ile Gln Ser Val 115 120 125

His Lys Asn Ala Phe Asn Asn Leu Lys Ala Arg Ala Arg Ile Ala Asn 130 135 140

Asn Pro Trp His Cys Asp Cys Thr Leu Gln Gln Val Leu Arg Ser Met 145 150 155 160

Ala Ser Asn His Glu Thr Ala His Asn Val Ile Cys Lys Thr Ser Val 165 170 175

Leu Asp Glu His Ala Gly Arg Pro Phe Leu Asn Ala Ala Asn Asp Ala 180 185 190

Asp Leu Cys Asn Leu Pro Lys Lys Thr Thr Asp Tyr Ala Met Leu Val 195 200 205

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Glu	Ala 210	Leu	Ser	His	Leu	His 215	Gly	Leu	Ile	Val	Leu 220	Arg	Leu	Arg	His
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Cys	Asn	Leu 275	Thr	Ala	Val	Pro	Tyr 280	Leu	Ala	Val	Arg	His 285	Leu	Val	Tyr
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Ser 305	Met	Leu	His	Glu	Leu 310	Leu	Arg	Leu	Gln	Glu 315	Ile	Gln	Leu	Val	Gly 320
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105

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115

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Thr Arg Ile Gln Glu Asp Pro Asn Gly Lys Thr Phe Thr Val Ser Ser 180 185 190

Ser Val Thr Phe Gln Val Thr Arg Glu Asp Asp Gly Ala Ser Ile Val 195 200 205

Cys Ser Val Asn His Glu Ser Leu Lys Gly Ala Asp Arg Ser Thr Ser 210 215 220

Gln Arg Ile Glu Val Leu Tyr Thr Pro Thr Ala Met Ile Arg Pro Asp 225 230 235 240

Pro Pro His Pro Arg Glu Gly Gln Lys Leu Leu His Cys Glu Gly 245 250 255

Arg Gly Asn Pro Val Pro Gln Gln Tyr Leu Trp Glu Lys Glu Gly Ser 260 265 270

Val Pro Pro Leu Lys Met Thr Gln Glu Ser Ala Leu Ile Phe Pro Phe 275 280 285

Leu Asn Lys Ser Asp Ser Gly Thr Tyr Gly Cys Thr Ala Thr Ser Asn 290 295 300

Met Gly Ser Tyr Lys Ala Tyr Tyr Thr Leu Asn Val Asn Asp Pro Ser 305 310 315 320

Pro Val Pro Ser Ser Ser Ser Thr Tyr His Ala Ile Ile Gly Gly Ile 325 330 335

Val Ala Phe Ile Val Phe Leu Leu Leu Ile Met Leu Ile Phe Leu Gly 340 345 350

His Tyr Leu Ile Arg His Lys Gly Thr Tyr Leu Thr His Glu Ala Lys 355 360 365

Gly Ser Asp Asp Ala Pro Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  $370 \hspace{1cm} 375 \hspace{1cm} 380$ 

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Val Pro Glu Gly Lys Val Val Leu Asn Phe Arg Phe Ile Asp Leu
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qcctctgata ctggagaata cagctgtgag qcacggaatg qgtatgqgac acccatgact 720
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<212> PRT
<213> Homo sapiens
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Leu Ala Ile Leu Cys Ser Leu Ala Leu Gly Ser Val Thr Val His
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Ser Cys Ala Tyr Ser Gly Phe Ser Ser Pro Arg Val Glu Trp Lys Phe
                         55
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<210> 118

Asp Gln Gly Asp Thr Thr Arg Leu Val Cys Tyr Asn Asn Lys Ile Thr 65 70 75 80

Ala Ser Tyr Glu Asp Arg Val Thr Phe Leu Pro Thr Gly Ile Thr Phe
85 90 95

Lys Ser Val Thr Arg Glu Asp Thr Gly Thr Tyr Thr Cys Met Val Ser 100 105 110

Glu Glu Gly Gly Asn Ser Tyr Gly Glu Val Lys Val Lys Leu Ile Val 115 120 125

Leu Val Pro Pro Ser Lys Pro Thr Val Asn Ile Pro Ser Ser Ala Thr 130 135 140

Ile Gly Asn Arg Ala Val Leu Thr Cys Ser Glu Gln Asp Gly Ser Pro145150155160

Pro Ser Glu Tyr Thr Trp Phe Lys Asp Gly Ile Val Met Pro Thr Asn 165 170 175

Pro Lys Ser Thr Arg Ala Phe Ser Asn Ser Ser Tyr Val Leu Asn Pro 180 185 190

Thr Thr Gly Glu Leu Val Phe Asp Pro Leu Ser Ala Ser Asp Thr Gly 195 200 205

Glu Tyr Ser Cys Glu Ala Arg Asn Gly Tyr Gly Thr Pro Met Thr Ser 210 215 220

Asn Ala Val Arg Met Glu Ala Val Glu Arg Asn Val Gly Val Ile Val 225 230 235 240

Ala Ala Val Leu Val Thr Leu Ile Leu Leu Gly Ile Leu Val Phe Gly 245 250 255

Ile Trp Phe Ala Tyr Ser Arg Gly His Phe Asp Arg Thr Lys Lys Gly 260 265 270

Thr Ser Ser Lys Lys Val Ile Tyr Ser Gln Pro Ser Ala Arg Ser Glu 275 280 285

Gly Glu Phe Lys Gln Thr Ser Ser Phe Leu Val 290 295

<210> 120

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<400> 120

tcgcggagct gtgttctgtt tccc

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<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
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<210> 122
<211> 20
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 122
acacctggtt caaagatggg
                                                                    20
<210> 123
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 123
taggaagagt tgctgaaggc acgg
                                                                    24
<210> 124
<211> 20
<212> DNA
<213> Artificial Sequence
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      oligonucleotide probe
<400> 124
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<210> 125
<211> 20
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
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<400> 125
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<210> 126
<211> 1210
<212> DNA
<213> Homo sapiens
<400> 126
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geetggagge egeegegage eegettteea eeeegacete tgeeeaggee geaggeeeea 180
geteaggete gtgcccacce accaagttee agtgccgcac cagtggetta tgcgtgcccc 240
tcacctggcg ctgcgacagg gacttggact gcagcgatgg cagcgatgag gaggagtgca 300
ggattgagec atgtacecag aaagggcaat geceaeegee eeetggeete eeetgeeeet 360
gcaccggcgt cagtgactgc tctgggggaa ctgacaagaa actgcgcaac tgcagccgcc 420
tggcctgcct agcaggcgag ctccgttgca cgctgagcga tgactgcatt ccactcacgt 480
ggcgctgcga cggccaccca gactgtcccg actccagcga cgagctcggc tgtggaacca 540
atgagatect eeeggaaggg gatgeeacaa eeatggggee eeetgtgace etggagagtg 600
tcacctctct caggaatgcc acaaccatgg ggccccctgt gaccctggag agtgtcccct 660
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gggttattgc agctgctgcg gtgctcagtg caagcctggt caccgccacc ctcctccttt 780
tgtcctggct ccgagcccag gagcgcctcc gcccactggg gttactggtg gccatgaagg 840
agtecetget getgteagaa eagaagaeet egetgeeetg aggaeaagea ettgeeacea 900
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gggcacacca gccctcagag acctgagttc ttctggccac gtggaacctc gaacccgagc 1020
teetgeagaa gtggeeetgg agattgaggg teeetggaea eteeetatgg agateegggg 1080
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aagttgcttc
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<211> 282
<212> PRT
<213> Homo sapiens
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Ala Ala Ala Ser Pro Leu Ser Thr Pro Thr Ser Ala Gln Ala Ala Gly
                             40
Pro Ser Ser Gly Ser Cys Pro Pro Thr Lys Phe Gln Cys Arg Thr Ser
     50
                         55
Gly Leu Cys Val Pro Leu Thr Trp Arg Cys Asp Arg Asp Leu Asp Cys
Ser Asp Gly Ser Asp Glu Glu Glu Cys Arg Ile Glu Pro Cys Thr Gln
                                     90
                 85
Lys Gly Gln Cys Pro Pro Pro Gly Leu Pro Cys Pro Cys Thr Gly
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100 105 110

Val Ser Asp Cys Ser Gly Gly Thr Asp Lys Lys Leu Arg Asn Cys Ser 115 120 125

Arg Leu Ala Cys Leu Ala Gly Glu Leu Arg Cys Thr Leu Ser Asp Asp 130 135 140

Cys Ile Pro Leu Thr Trp Arg Cys Asp Gly His Pro Asp Cys Pro Asp 145 150 155 160

Ser Ser Asp Glu Leu Gly Cys Gly Thr Asn Glu Ile Leu Pro Glu Gly 165 170 175

Asp Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val Thr Ser 180 185 190

Leu Arg Asn Ala Thr Thr Met Gly Pro Pro Val Thr Leu Glu Ser Val 195 200 205

Pro Ser Val Gly Asn Ala Thr Ser Ser Ser Ala Gly Asp Gln Ser Gly 210 215 220

Ser Pro Thr Ala Tyr Gly Val Ile Ala Ala Ala Ala Val Leu Ser Ala 225 230 235 240

Ser Leu Val Thr Ala Thr Leu Leu Leu Leu Ser Trp Leu Arg Ala Gln 245 250 255

Glu Arg Leu Arg Pro Leu Gly Leu Leu Val Ala Met Lys Glu Ser Leu 260 265 270

Leu Leu Ser Glu Gln Lys Thr Ser Leu Pro 275 280

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<400> 128

aagttccagt gccgcaccag tggc

24

<210> 129

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 oligonucleotide probe

<400> 129

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24
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<210> 130
<211> 50
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 130
                                                                   50
gaggaggagt gcaggattga gccatgtacc cagaaagggc aatgcccacc
<210> 131
<211> 1843
<212> DNA
<213> Homo sapiens
<220>
<221> modified base
<222> (1837)..(1837)
<223> a, t, c or g
<400> 131
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cagactettg caagetggat geeetetgtg gatgaaagat gtateatgga atgaaceega 180
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 ctgatcctta aaattgctat gctgatagag tggtgagggc tggaagcttg atcaagtcct 1800
                                                                   1843
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<210>	132
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<212>	PRT

<213> Homo sapiens

<400> 132

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Ile Leu Trp Phe Gln Leu Ala Leu Cys Phe Gly Pro Ala Gln Leu Thr

Gly Gly Phe Asp Asp Leu Gln Val Cys Ala Asp Pro Gly Ile Pro Glu

Asn Gly Phe Arg Thr Pro Ser Gly Gly Val Phe Phe Glu Gly Ser Val

Ala Arg Phe His Cys Gln Asp Gly Phe Lys Leu Lys Gly Ala Thr Lys 85

Arg Leu Cys Leu Lys His Phe Asn Gly Thr Leu Gly Trp Ile Pro Ser 105

Asp Asn Ser Ile Cys Val Gln Glu Asp Cys Arg Ile Pro Gln Ile Glu

Asp Ala Glu Ile His Asn Lys Thr Tyr Arg His Gly Glu Lys Leu Ile

Ile Thr Cys His Glu Gly Phe Lys Ile Arg Tyr Pro Asp Leu His Asn

Met Val Ser Leu Cys Arg Asp Asp Gly Thr Trp Asn Asn Leu Pro Ile 170 165

Cys Gln Gly Cys Leu Arg Pro Leu Ala Ser Ser Asn Gly Tyr Val Asn 185

Ile Ser Glu Leu Gln Thr Ser Phe Pro Val Gly Thr Val Ile Ser Tyr

Arg Cys Phe Pro Gly Phe Lys Leu Asp Gly Ser Ala Tyr Leu Glu Cys 215

Leu Gln Asn Leu Ile Trp Ser Ser Ser Pro Pro Arg Cys Leu Ala Leu 230

Glu Ala Gln Val Cys Pro Leu Pro Pro Met Val Ser His Gly Asp Phe 245

Val Cys His Pro Arg Pro Cys Glu Arg Tyr Asn His Gly Thr Val Val 265

Glu Phe Tyr Cys Asp Pro Gly Tyr Ser Leu Thr Ser Asp Tyr Lys Tyr 275 280 285

Ile Thr Cys Gln Tyr Gly Glu Trp Phe Pro Ser Tyr Gln Val Tyr Cys 290 295 300

Ile Lys Ser Glu Gln Thr Trp Pro Ser Thr His Glu Thr Leu Leu Thr 305 310 315 320

Thr Trp Lys Ile Val Ala Phe Thr Ala Thr Ser Val Leu Leu Val Leu 325 330 335

Leu Leu Val Ile Leu Ala Arg Met Phe Gln Thr Lys Phe Lys Ala His 340 . 345 350

Phe Pro Pro Arg Gly Pro Pro Arg Ser Ser Ser Ser Asp Pro Asp Phe 355 360 365

Val Val Val Asp Gly Val Pro Val Met Leu Pro Ser Tyr Asp Glu Ala 370 375 380

Val Ser Gly Gly Leu Ser Ala Leu Gly Pro Gly Tyr Met Ala Ser Val 385 390 395

Gly Gln Gly Cys Pro Leu Pro Val Asp Asp Gln Ser Pro Pro Ala Tyr 405 410 415

Pro Gly Ser Gly Asp Thr Asp Thr Gly Pro Gly Glu Ser Glu Thr Cys 420 425 430

Asp Ser Val Ser Gly Ser Ser Glu Leu Leu Gln Ser Leu Tyr Ser Pro

Pro Arg Cys Gln Glu Ser Thr His Pro Ala Ser Asp Asn Pro Asp Ile 450 455 460

Ile Ala Ser Thr Ala Glu Glu Val Ala Ser Thr Ser Pro Gly Ile His 465 470 475 480

His Ala His Trp Val Leu Phe Leu Arg Asn 485 490

<210> 133

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<400> 133

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<210> 134

<211> 23

<212> DNA

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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 134
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                                                                   23
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<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Synthetic
      oligonucleotide probe
<400> 135
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<210> 136
<211> 1815
<212> DNA
<213> Homo sapiens
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ccgtagcgcc cgagtgtcgg ggggcgcacc cgagtcgqgc catqagqccq qqaaccqcqc 180
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ggccttgtta taaagtcatt tacttccatg atacttctcg aagactgaac tttgaggaag 360
ccaaagaagc ctgcaggagg gatggaggcc agctagtcag catcgagtct gaagatgaac 420
agaaactgat agaaaagttc attgaaaacc tcttgccatc tgatggtgac ttctggattg 480
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ggactgatgg cagcatatca caatttagga actggtatgt ggatgagccg tcctgcggca 600
gcgaggtctg cgtggtcatg taccatcagc catcggcacc cgctggcatc ggaggcccct 660
acatgttcca gtggaatgat gaccggtgca acatgaagaa caatttcatt tgcaaatatt 720
ctgatgagaa accagcagtt ccttctagag aagctgaagg tgaggaaaca gagctgacaa 780
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gagaagctgc cttgaatctg gcctacatcc taatccccag cattcccctt ctcctcctcc 900
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cagaccctag cacaaagaag caacaccca tctggccctc tcctcaccag ggaaacagcc 1020
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ggccagacct gaagaatatt tcattccgag tgtgttcggg agaagccact cccgatgaca 1140
tgtcttgtga ctatgacaac atggctgtga acccatcaga aagtgggttt gtgactctgg 1200
tgagcgtgga gagtggattt gtgaccaatg acatttatga gttctcccca gaccaaatgg 1260
ggaggagtaa ggagtctgga tgggtggaaa atgaaatata tggttattag gacatataaa 1320
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ggaaaataca cagaaggtct atgaacaagc ttagatcagg tcctgtggat gagcatgtgg 1440
tececaegae etectgttgg acceeeagt tttggetgta teetttatee eageeagtea 1500
tccagctcga ccttatgaga aggtaccttg cccaggtctg gcacatagta gagtctcaat 1560
aaatgtcact tggttggttg tatctaactt ttaagggaca gagctttacc tggcagtgat 1620
aaagatgggc tqtggagctt ggaaaaccac ctctqttttc cttqctctat acagcagcac 1680
atattatcat acagacagaa aatccagaat cttttcaaag cccacatatg gtagcacagg 1740
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- <210> 137
- <211> 382
- <212> PRT
- <213> Homo sapiens
- <400> 137
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- Val Gly Leu Arg Ala Ala Thr Gly Arg Leu Leu Ser Ala Ser Asp Leu 20 25 30
- Asp Leu Arg Gly Gly Gln Pro Val Cys Arg Gly Gly Thr Gln Arg Pro 35 40 45
- Cys Tyr Lys Val Ile Tyr Phe His Asp Thr Ser Arg Arg Leu Asn Phe 50 55 60
- Glu Glu Ala Lys Glu Ala Cys Arg Arg Asp Gly Gly Gln Leu Val Ser 65 70 75 80
- Ile Glu Ser Glu Asp Glu Gln Lys Leu Ile Glu Lys Phe Ile Glu Asn 85 90 95
- Leu Leu Pro Ser Asp Gly Asp Phe Trp Ile Gly Leu Arg Arg Glu
  100 105 110
- Glu Lys Gln Ser Asn Ser Thr Ala Cys Gln Asp Leu Tyr Ala Trp Thr 115 120 125
- Asp Gly Ser Ile Ser Gln Phe Arg Asn Trp Tyr Val Asp Glu Pro Ser 130 135 140
- Cys Gly Ser Glu Val Cys Val Val Met Tyr His Gln Pro Ser Ala Pro 145 150 155 160
- Ala Gly Ile Gly Gly Pro Tyr Met Phe Gln Trp Asn Asp Asp Arg Cys 165 170 175
- Asn Met Lys Asn Asn Phe Ile Cys Lys Tyr Ser Asp Glu Lys Pro Ala 180 185 190
- Val Pro Ser Arg Glu Ala Glu Gly Glu Glu Thr Glu Leu Thr Thr Pro 195 200 205
- Val Leu Pro Glu Glu Thr Gln Glu Glu Asp Ala Lys Lys Thr Phe Lys 210 215 220
- Glu Ser Arg Glu Ala Ala Leu Asn Leu Ala Tyr Ile Leu Ile Pro Ser 225 230 235 240
- Ile Pro Leu Leu Leu Leu Val Val Thr Thr Val Val Cys Trp Val 245 250 255
- Trp Ile Cys Arg Lys Arg Lys Arg Glu Gln Pro Asp Pro Ser Thr Lys

			260					265					270			
Lys	Gln	His 275	Thr	Ile	Trp	Pro	Ser 280	Pro	His	Gln	Gly	Asn 285	Ser	Pro	Asp	
Leu	Glu 290	Val	Tyr	Asn	Val	Ile 295	Arg	Lys	Gln	Ser	Glu 300	Ala	Asp	Leu	Ala	
Glu 305	Thr	Arg	Pro	Asp	Leu 310	Lys	Asn	Ile	Ser	Phe 315	Arg	Val	Cys	Ser	Gly 320	
Glu	Ala	Thr	Pro	Asp 325	Asp	Met	Ser	Cys	Asp 330	Tyr	Asp	Asn	Met	Ala 335	Val	
Asn	Pro	Ser	Glu 340	Ser	Gly	Phe	Val	Thr 345	Leu	Val	Ser	Val	Glu 350	Ser	Gly	
Phe	Val	Thr 355	Asn	Asp	Ile	Tyr	Glu 360	Phe	Ser	Pro	Asp	Gln 365	Met	Gly	Arg	
Ser	Lys 370	Glu	Ser	Gly	Trp	Val 375	Glu	Asn	Glu	Ile	Tyr 380	Gly	Tyr			
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<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe																
	)> 13 catto		acct	ctt	jc ca	atcto	gatgo	g tga	actto	ctgg	att	gggct	ca			50
<210> 139 <211> 24 <212> DNA <213> Artificial Sequence																
<220> <223> Description of Artificial Sequence: Synthetic oligonucleotide probe																
	)> 13 ccaaa	_	agcct	cgcaç	gg ag	133										24
<211 <212	)> 14 l> 24 2> Di 3> Ar	l 1A	cial	l Sec	quenc	ce										
	<213> Artificial Sequence  <220>  <223> Description of Artificial Sequence: Synthetic oligonucleotide probe															

<400> 140

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<210> 141
<211> 1514
<212> DNA
<213> Homo sapiens
<400> 141
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ttgtgtttgc ctcctgcagc ctcaacccgg agggcagcga gggcctacca ccatgatcac 180
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cctgcaccag cggcggttgg ccctggccga gctgcaggag gccgatggcc agtqtccqgt 300
cgaccgcagc ctgctgaagt tgaaaatggt gcaggtcgtg tttcgacacg gggctcggag 360
tecteteaag eegeteeege tggaggagea ggtagagtgg aacceeeage tattagaggt 420
cccaccccaa actcagtttg attacacagt caccaatcta gctggtggtc cgaaaccata 480
ttctccttac gactctcaat accatgagac caccctgaag gggggcatgt ttgctgggca 540
gctgaccaag gtgggcatgc agcaaatgtt tgccttggga gagagactga ggaagaacta 600
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cactaacatt tttcggaatc tggagtccac ccgttgtttg ctggctgggc ttttccagtg 720
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Glu Leu Gln Glu Ala Asp Gly Gln Cys Pro Val Asp Arg Ser Leu Leu
Lys Leu Lys Met Val Gln Val Val Phe Arg His Gly Ala Arg Ser Pro
Leu Lys Pro Leu Pro Leu Glu Glu Gln Val Glu Trp Asn Pro Gln Leu
                     70
                                         75
Leu Glu Val Pro Pro Gln Thr Gln Phe Asp Tyr Thr Val Thr Asn Leu
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Ala Gly Gly Pro Lys Pro Tyr Ser Pro Tyr Asp Ser Gln Tyr His Glu 100 105 Thr Thr Leu Lys Gly Gly Met Phe Ala Gly Gln Leu Thr Lys Val Gly 120 Met Gln Gln Met Phe Ala Leu Gly Glu Arg Leu Arg Lys Asn Tyr Val Glu Asp Ile Pro Phe Leu Ser Pro Thr Phe Asn Pro Gln Glu Val Phe 150 155 Ile Arg Ser Thr Asn Ile Phe Arg Asn Leu Glu Ser Thr Arg Cys Leu 170 Leu Ala Gly Leu Phe Gln Cys Gln Lys Glu Gly Pro Ile Ile His 180 185 Thr Asp Glu Ala Asp Ser Glu Val Leu Tyr Pro Asn Tyr Gln Ser Cys 200 Trp Ser Leu Arg Gln Arg Thr Arg Gly Arg Arg Gln Thr Ala Ser Leu 220 Gln Pro Gly Ile Ser Glu Asp Leu Lys Lys Val Lys Asp Arg Met Gly 230 Ile Asp Ser Ser Asp Lys Val Asp Phe Phe Ile Leu Leu Asp Asn Val 250 245 Ala Ala Glu Gln Ala His Asn Leu Pro Ser Cys Pro Met Leu Lys Arg 260 Phe Ala Arg Met Ile Glu Gln Arg Ala Val Asp Thr Ser Leu Tyr Ile 280 Leu Pro Lys Glu Asp Arg Glu Ser Leu Gln Met Ala Val Gly Pro Phe 290 295 Leu His Ile Leu Glu Ser Asn Leu Leu Lys Ala Met Asp Ser Ala Thr 310 Ala Pro Asp Lys Ile Arg Lys Leu Tyr Leu Tyr Ala Ala His Asp Val 330 335 Thr Phe Ile Pro Leu Leu Met Thr Leu Gly Ile Phe Asp His Lys Trp Pro Pro Phe Ala Val Asp Leu Thr Met Glu Leu Tyr Gln His Leu Glu 360 Ser Lys Glu Trp Phe Val Gln Leu Tyr Tyr His Gly Lys Glu Gln Val 370 Pro Arg Gly Cys Pro Asp Gly Leu Cys Pro Leu Asp Met Phe Leu Asn

385	390	395		400							
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cettqccatt tqcaccaqae etqqatteet aqeqteteca tetqqaqtqe qqetqqtqqq 180
gggcctccac cgctgtgaag ggcgggtgga ggtggaacag aaaggccagt ggggcaccqt 240
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agaagaagtt tatgattgtt cacatgatga agatgctggg gcatcgtgtg agaacccaga 480
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acqqaatttt aaqqataaat tttctqaatt qqttatqqqq tttctqaaat tqqctctata 1620
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<211> 347
<212> PRT
<213> Homo sapiens
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Phe Leu Ala Ser Pro Ser Gly Val Arg Leu Val Gly Gly Leu His Arg
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Cys Glu Gly Arg Val Glu Val Glu Gln Lys Gly Gln Trp Gly Thr Val
Cys Asp Asp Gly Trp Asp Ile Lys Asp Val Ala Val Leu Cys Arg Glu
                         55
Leu Gly Cys Gly Ala Ala Ser Gly Thr Pro Ser Gly Ile Leu Tyr Glu
 65
                     70
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Pro Pro Ala Glu Lys Glu Gln Lys Val Leu Ile Gln Ser Val Ser Cys

Thr Gly Thr Glu Asp Thr Leu Ala Gln Cys Glu Gln Glu Glu Val Tyr 105 Asp Cys Ser His Asp Glu Asp Ala Gly Ala Ser Cys Glu Asn Pro Glu 120 Ser Ser Phe Ser Pro Val Pro Glu Gly Val Arg Leu Ala Asp Gly Pro 130 140 Gly His Cys Lys Gly Arg Val Glu Val Lys His Gln Asn Gln Trp Tyr 150 155 Thr Val Cys Gln Thr Gly Trp Ser Leu Arg Ala Ala Lys Val Val Cys 170 Arg Gln Leu Gly Cys Gly Arg Ala Val Leu Thr Gln Lys Arg Cys Asn 185 Lys His Ala Tyr Gly Arg Lys Pro Ile Trp Leu Ser Gln Met Ser Cys 200 Ser Gly Arg Glu Ala Thr Leu Gln Asp Cys Pro Ser Gly Pro Trp Gly 210 215 220 Lys Asn Thr Cys Asn His Asp Glu Asp Thr Trp Val Glu Cys Glu Asp 230 Pro Phe Asp Leu Arg Leu Val Gly Gly Asp Asn Leu Cys Ser Gly Arg 250 Leu Glu Val Leu His Lys Gly Val Trp Gly Ser Val Cys Asp Asp Asn Trp Gly Glu Lys Glu Asp Gln Val Val Cys Lys Gln Leu Gly Cys Gly 280 Lys Ser Leu Ser Pro Ser Phe Arg Asp Arg Lys Cys Tyr Gly Pro Gly 300 290 295 Val Gly Arg Ile Trp Leu Asp Asn Val Arg Cys Ser Gly Glu Glu Gln 305 Ser Leu Glu Gln Cys Gln His Arg Phe Trp Gly Phe His Asp Cys Thr 330

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<212> DNA

<213> Artificial Sequence

340

<220>

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345

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## oligonucleotide probe

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<213> Homo sapiens
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qaaqqtgaaq gccatggact tcatcacctc cacagccatc ctgcccctgc tgttcggctg 180
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gctcatcaga gaacttaccg cttctcatgc caccaaggtg cagacacaca agccttactt 420
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gtgctttggc tatgtcgaca tacttgtcaa caatgctggg atcagctacc gtggtaccat 540
catggacacc acagtggatg tggacaagag ggtcatggag acaaactact ttggcccagt 600
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catcagcage atccagggea agatgageat teettttega teagcatatg cageeteeaa 720
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<211> 310

<212> PRT

<213> Homo sapiens

<400> 153

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Ala Tyr Leu Arg Asn Ala Val Val Ile Thr Gly Ala Thr Ser Gly 35 40 45

Leu Gly Lys Glu Cys Ala Lys Val Phe Tyr Ala Ala Gly Ala Lys Leu 50 55 60

Val Leu Cys Gly Arg Asn Gly Gly Ala Leu Glu Glu Leu Ile Arg Glu 65 70 75 80

Leu Thr Ala Ser His Ala Thr Lys Val Gln Thr His Lys Pro Tyr Leu

85 90 95

Val Thr Phe Asp Leu Thr Asp Ser Gly Ala Ile Val Ala Ala Ala Ala 100 105 110

Glu Ile Leu Gln Cys Phe Gly Tyr Val Asp Ile Leu Val Asn Asn Ala 115 120 125

Gly Ile Ser Tyr Arg Gly Thr Ile Met Asp Thr Thr Val Asp Val Asp 130 135 140

Lys Arg Val Met Glu Thr Asn Tyr Phe Gly Pro Val Ala Leu Thr Lys 145 150 155 160

Ala Leu Leu Pro Ser Met Ile Lys Arg Arg Gln Gly His Ile Val Ala 165 170 175

Ile Ser Ser Ile Gln Gly Lys Met Ser Ile Pro Phe Arg Ser Ala Tyr 180 185 190

Ala Ala Ser Lys His Ala Thr Gln Ala Phe Phe Asp Cys Leu Arg Ala 195 200 205

Glu Met Glu Gln Tyr Glu Ile Glu Val Thr Val Ile Ser Pro Gly Tyr 210 215 220

Ile His Thr Asn Leu Ser Val Asn Ala Ile Thr Ala Asp Gly Ser Arg 225 230 235 240

Tyr Gly Val Met Asp Thr Thr Thr Ala Gln Gly Arg Ser Pro Val Glu 245 250 255

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Val Ala Gln Asp Val Leu Ala Ala Val Gly Lys Lys Lys Asp Val
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Ile Leu Ala Asp Leu Leu Pro Ser Leu Ala Val Tyr Leu Arg Thr Leu
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Arg Lys Ser Lys Asn Ser
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Gly Arg Leu Thr Ala Tyr Glu Phe Ala Lys Leu Lys Ser Lys Leu Val
                         55
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Leu Trp Asp Ile Asn Lys His Gly Leu Glu Glu Thr Ala Ala Lys Cys 65 70 75 80

Lys Gly Leu Gly Ala Lys Val His Thr Phe Val Val Asp Cys Ser Asn 85 90 95

Arg Glu Asp Ile Tyr Ser Ser Ala Lys Lys Val Lys Ala Glu Ile Gly
100 105 110

Asp Val Ser Ile Leu Val Asn Asn Ala Gly Val Val Tyr Thr Ser Asp 115 120 125

Leu Phe Ala Thr Gln Asp Pro Gln Ile Glu Lys Thr Phe Glu Val Asn 130 135 140

Val Leu Ala His Phe Trp Thr Thr Lys Ala Phe Leu Pro Ala Met Thr 145 150 155 160

Lys Asn Asn His Gly His Ile Val Thr Val Ala Ser Ala Ala Gly His 165 170 175

Val Ser Val Pro Phe Leu Leu Ala Tyr Cys Ser Ser Lys Phe Ala Ala 180 185 190

Val Gly Phe His Lys Thr Leu Thr Asp Glu Leu Ala Ala Leu Gln Ile 195 200 205

Thr Gly Val Lys Thr Thr Cys Leu Cys Pro Asn Phe Val Asn Thr Gly 210 215 220

Phe Ile Lys Asn Pro Ser Thr Ser Leu Gly Pro Thr Leu Glu Pro Glu 225 230 235 240

Glu Val Val Asn Arg Leu Met His Gly Ile Leu Thr Glu Gln Lys Met 245 250 255

Ile Phe Ile Pro Ser Ser Ile Ala Phe Leu Thr Thr Leu Glu Arg Ile 260 265 270

Leu Pro Glu Arg Phe Leu Ala Val Leu Lys Arg Lys Ile Ser Val Lys 275 280 285

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<400> 160

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Ile Glu Ala Gly Lys Ile Gln Lys Gly Arg Glu Leu Ser Leu Val Gly
Pro Phe Pro Gly Leu Asn Met Lys Ser Tyr Ala Gly Phe Leu Thr Val
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Asn Lys Thr Tyr Asn Ser Asn Leu Phe Phe Trp Phe Phe Pro Ala Gln
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Gly Gly Ser Ser Met Phe Gly Leu Phe Val Glu His Gly Pro Tyr Val
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Val Thr Ser Asn Met Thr Leu Arg Asp Arg Asp Phe Pro Trp Thr Thr
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Thr Leu Ser Met Leu Tyr Ile Asp Asn Pro Val Gly Thr Gly Phe Ser
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Phe Thr Asp Asp Thr His Gly Tyr Ala Val Asn Glu Asp Asp Val Ala
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Arg Asp Leu Tyr Ser Ala Leu Ile Gln Phe Phe Gln Ile Phe Pro Glu
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Tyr Lys Asn Asn Asp Phe Tyr Val Thr Gly Glu Ser Tyr Ala Gly Lys
Tyr Val Pro Ala Ile Ala His Leu Ile His Ser Leu Asn Pro Val Arg
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215

210

Glu Val Lys Ile Asn Leu Asn Gly Ile Ala Ile Gly Asp Gly Tyr Ser 225 230 235 240

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245 250 255

Gly Leu Leu Asp Glu Lys Gln Lys Lys Tyr Phe Gln Lys Gln Cys His
260 265 270

Glu Cys Ile Glu His Ile Arg Lys Gln Asn Trp Phe Glu Ala Phe Glu 275 280 285

Ile Leu Asp Lys Leu Leu Asp Gly Asp Leu Thr Ser Asp Pro Ser Tyr 290 295 300

Phe Gln Asn Val Thr Gly Cys Ser Asn Tyr Tyr Asn Phe Leu Arg Cys 305 310 315 320

Thr Glu Pro Glu Asp Gln Leu Tyr Tyr Val Lys Phe Leu Ser Leu Pro 325 330 335

Glu Val Arg Gln Ala Ile His Val Gly Asn Gln Thr Phe Asn Asp Gly 340 345 350

Thr Ile Val Glu Lys Tyr Leu Arg Glu Asp Thr Val Gln Ser Val Lys 355 360 365

Pro Trp Leu Thr Glu Ile Met Asn Asn Tyr Lys Val Leu Ile Tyr Asn 370 375 380

Gly Gln Leu Asp Ile Ile Val Ala Ala Ala Leu Thr Glu Arg Ser Leu 385 390 395 400

Met Gly Met Asp Trp Lys Gly Ser Gln Glu Tyr Lys Lys Ala Glu Lys 405 410 415

Lys Val Trp Lys Ile Phe Lys Ser Asp Ser Glu Val Ala Gly Tyr Ile 420 425 430

Arg Gln Ala Gly Asp Phe His Gln Val Ile Ile Arg Gly Gly His 435 440 445

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Gln Pro Gly Lys Val Glu Gln Met Ser Thr His Arg Ser Arg Leu Leu
Thr Ala Ala Pro Leu Ser Met Glu Gln Arg Gln Pro Trp Pro Arg Ala
                         55
Leu Glu Val Asp Ser Arg Ser Val Val Leu Leu Ser Val Val Trp Val
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Leu Leu Ala Pro Pro Ala Ala Gly Met Pro Gln Phe Ser Thr Phe His

Ser Glu Asn Arg Asp Trp Thr Phe Asn His Leu Thr Val His Gln Gly

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His His Pro Pro Asp Asp Ser Ala Leu Cys Ala Phe Pro Ile Arg Ala

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	Gly	Asn	Leu 435	Glu	Leu	Asn	Trp	Leu 440	Leu	Gly	Lys	Asp	Val 445	Gln	Cys	Thr	
	Lys	Ala 450	Pro	Val	Pro	Ile	Asp 455	Asp	Asn	Phe	Cys	Gly 460	Leu	Asp	Ile	Asn	
	Gln 465	Pro	Leu	Gly	Gly	Ser 470	Thr	Pro	Val	Glu	Gly 475	Leu	Thr	Leu	Tyr	Thr 480	
	Thr	Ser	Arg	Asp	Arg 485	Met	Thr	Ser	Val	Ala 490	Ser	Tyr	Val	Tyr	Asn 495	Gly	
	Tyr	Ser	Val	Val 500	Phe	Val	Gly	Thr	Lys 505	Ser	Gly	Lys	Leu	Lys 510	Lys	Val	
	Arg	Val	Tyr 515	Glu	Phe	Arg	Cys	Ser 520	Asn	Ala	Ile	His	Leu 525	Leu	Ser	Lys	
	Glu	Ser 530	Leu	Leu	Glu	Gly	Ser 535	Tyr	Trp	Trp	Arg	Phe 540	Asn	Tyr	Arg	Gln	
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Tyr	Glu	Thr 435		Ile	Thr	Ser	Ser 440		lle	Leu	Ser	Gly 445	His	Val	His
Asp	Arg 450		Gln	Val	Phe	Val 455		Thr	· Val	Ser	Ile 460		Phe	Leu	Asp

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Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Set Thr
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Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val
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Val Phe Asp Leu Thr Asp Leu Asp Val Leu Lys Leu Glu Leu Ile Pro 130 135 140

Glu Ala Lys Ile Pro Ala Lys Ile Ser Gln Met Thr Asn Leu Gln Glu 145 150 155 160

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Glu Ser Leu Arg Glu Leu Arg His Leu Lys Ile Leu His Val Lys Ser 235 230 235

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Thr Lys Leu Val Ile His Asn Asp Gly Thr Lys Leu Leu Val Leu Asn 260 265 270

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Ser Phe Gln His Leu Lys Arg Leu Thr Cys Leu Lys Leu Trp His Asn 325 330 335

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Ser Ser Asn Gly Pro Leu Leu Gly Gln Val Cys Ser Lys Asn Asp Tyr 100 105 110

Val Pro Val Phe Glu Ser Ser Ser Ser Thr Leu Thr Phe Gln Ile Val 115 120 125

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Leu Glu Gly Ser Phe Thr Ser Pro Asn Tyr Pro Lys Pro His Pro Glu 165 170 175

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Lys Leu Asn Phe Lys Glu Ile Phe Leu Glu Ile Asp Lys Gln Cys Lys 195 200 205

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Gly Leu Ser Leu Ala Gly Lys Asp Gln Val Glu Thr Ala Leu Lys Ala 65 70 75 80

Ser Phe Glu Thr Cys Ser Tyr Gly Trp Val Gly Asp Gly Phe Val Val 85 90 95

Ile Ser Arg Ile Ser Pro Asn Pro Lys Cys Gly Lys Asn Gly Val Gly 100 105 110

Val Leu Ile Trp Lys Val Pro Val Ser Arg Gln Phe Ala Ala Tyr Cys 115 120 125

Tyr Asn Ser Ser Asp Thr Trp Thr Asn Ser Cys Ile Pro Glu Ile Ile 130 135 140

Thr Thr Lys Asp Pro Ile Phe Asn Thr Gln Thr Ala Thr Gln Thr Thr 145 150 155 160

Glu Phe Ile Val Ser Asp Ser Thr Tyr Ser Val Ala Ser Pro Tyr Ser 165 170 175

Thr Ile Pro Ala Pro Thr Thr Thr Pro Pro Ala Pro Ala Ser Thr Ser 180 185 190

Ile Pro Arg Arg Lys Lys Leu Ile Cys Val Thr Glu Val Phe Met Glu 195 200 205

Thr Ser Thr Met Ser Thr Glu Thr Glu Pro Phe Val Glu Asn Lys Ala 210 215 220

Ala Phe Lys Asn Glu Ala Ala Gly Phe Gly Gly Val Pro Thr Ala Leu 225 230 235 240

Leu Val Leu Ala Leu Leu Phe Phe Gly Ala Ala Ala Gly Leu Gly Phe 245 250 255

Cys Tyr Val Lys Arg Tyr Val Lys Ala Phe Pro Phe Thr Asn Lys Asn

260 265 270

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Leu Pro Thr Gln Arg Glu Asp Gly Asn Pro Cys Asp Phe Asp Trp Arg 50 55 60

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Arg Arg Ser Ile Thr Val Glu Gln His Ile Gly Asn Ile Phe Met Phe 85 90 95

Ser Lys Val Ala Asn Thr Ile Leu Phe Phe Arg Leu Asp Ile Arg Met 100 105 110

Gly Leu Leu Tyr Ile Thr Leu Cys Ile Val Phe Leu Met Thr Cys Lys 115 120 125

Pro Pro Leu Tyr Met Gly Pro Glu Tyr Ile Lys Tyr Phe Asn Asp Lys 130 135 140

Thr Ile Asp Glu Glu Leu Glu Arg Asp Lys Arg Val Thr Trp Ile Val 145 150 155 160

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Tyr Ala Asp Leu Ser Leu Lys Tyr Asn Cys Thr Gly Leu Asn Phe Gly
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Lys Val Asp Val Gly Arg Tyr Thr Asp Val Ser Thr Arg Tyr Lys Val 195 200 205

Ser Thr Ser Pro Leu Thr Lys Gln Leu Pro Thr Leu Ile Leu Phe Gln 210 215 220

Gly Gly Lys Glu Ala Met Arg Arg Pro Gln Ile Asp Lys Lys Gly Arg 225 230 235 240

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55

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- Val Ser Leu Ala Glu Leu Arg Ala Trp Ile Ala His Thr Gln Gln Arg 100 105 110
- His Ile Arg Asp Ser Val Ser Ala Ala Trp Asp Thr Tyr Asp Thr Asp 115 120 125
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- Tyr Lys Lys Met Leu Ala Arg Asp Glu Arg Arg Phe Arg Val Ala Asp 165 170 175
- Gln Asp Gly Asp Ser Met Ala Thr Arg Glu Glu Leu Thr Ala Phe Leu 180 185 190
- His Pro Glu Glu Phe Pro His Met Arg Asp Ile Val Ile Ala Glu Thr 195 200 205
- Leu Glu Asp Leu Asp Arg Asn Lys Asp Gly Tyr Val Gln Val Glu Glu 210 215 220
- Tyr Ile Ala Asp Leu Tyr Ser Ala Glu Pro Gly Glu Glu Glu Pro Ala 225 230 235 240
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- Lys Asp Gly His Leu Asp Gly Ser Glu Val Gly His Trp Val Leu Pro 260 265 270
- Pro Ala Gln Asp Gln Pro Leu Val Glu Ala Asn His Leu Leu His Glu 275 280 285
- Ser Asp Thr Asp Lys Asp Gly Arg Leu Ser Lys Ala Glu Ile Leu Gly 290 295 300
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Asp Ile Gly Ala Lys Ile Ala Ala Val Gln Phe Thr Tyr Asp Gln Arg 405 410 415

Thr Glu Phe Ser Phe Thr Asp Tyr Ser Thr Lys Glu Asn Val Leu Ala 420 425 430

Val Ile Arg Asn Ile Arg Tyr Met Ser Gly Gly Thr Ala Thr Gly Asp 435 440 445

Ala Ile Ser Phe Thr Val Arg Asn Val Phe Gly Pro Ile Arg Glu Ser 450 455 460

Pro Asn Lys Asn Phe Leu Val Ile Val Thr Asp Gly Gln Ser Tyr Asp 465 470 475 480

Asp Val Gln Gly Pro Ala Ala Ala Ala His Asp Ala Gly Ile Thr Ile 485 490 495

Phe Ser Val Gly Val Ala Trp Ala Pro Leu Asp Asp Leu Lys Asp Met 500 505 510

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<213> Homo sapiens

<400> 236

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Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys 65 70 75 80

Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
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Glu Thr Asn Thr Asp Thr Lys Val Gly Asn Asn Thr Ile His Val His

Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe 115 120 125

Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser 130 135 140

His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln 145 150 155 160

Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met 165 170 175

Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp 180 185 190

Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys 195 200 205

Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220

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Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255

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Thr Ala Val Pro Pro Ala Leu Pro Ala Gly Thr Gln Thr Leu Leu 65 70 75

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Tyr Leu Ala Asn Leu Thr Glu Leu Asp Leu Ser Gln Asn Ser Phe 95 100 105

Ser Asp Ala Arg Asp Cys Asp Phe His Ala Leu Pro Gln Leu Leu 110 115 120

Ser Leu His Leu Glu Glu Asn Gln Leu Thr Arg Leu Glu Asp His 125 130 135

Ser Phe Ala Gly Leu Ala Ser Leu Gln Glu Leu Tyr Leu Asn His 140 145 150

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Asp	Ser	Arg	Trp	Phe 185		Met	Leu	Pro	Asn 190		Glu	ılle	Leu	Met 195
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His	Leu	Lys	Glu	Leu 290	Gly	Leu	Asn	Asn	Met 295	Glu	Glu	Leu	Val	Ser 300
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Glu	Pro	Gln	Ser	Thr 395	Leu	Cys	Ala	Glu	Pro 400	Pro	Asp	Leu	Gln	Arg 405
Leu	Pro	Val	Arg	Glu 410	Val	Pro	Phe	Arg	Glu 415	Met	Thr	Asp	His	Cys 420
Leu	Pro	Leu	Ile	Ser 425	Pro	Arg	Ser	Phe	Pro 430	Pro	Ser	Leu	Gln	Val 435

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Ser	Val	Val	Val	Gly 515	Arg	Ala	Leu	Leu	Gln 520	Pro	Gly	Arg	Asp	Glu 525
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Leu	Thr	Trp	Ser	Ser 560	Ala	Ser	Ser	Leu	Arg 565	Gly	Gln	Gly	Ala	Thr 570
Ala	Leu	Ala	Arg	Leu 575	Pro	Arg	Gly	Thr	His 580	Ser	Tyr	Asn	Ile	Thr 58,5
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Phe	Ala	Asp	Ala	His 605	Thr	Gln	Leu	Ala	Cys 610	Val	Trp	Ala	Arg	Thr 615
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Gly	Arg	Arg	Pro	Leu 665	Pro	Pro	Ala	Trp	Ala 670	Phe	Trp	Gly	Trp	Ser 675
Ala	Pro	Ser	Val	Arg 680	Val	Val	Ser	Ala	Pro 685	Leu	Val	Leu	Pro	Trp 690
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Trp Leu Tyr His Thr Ala Ala Lys Ile Glu Ala Pro Ala Leu Ala

205

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<213> Homo Sapien
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Trp	Pro	Thr	Glu	Glu 35	Gly	Lys	Glu	Val	Trp 40	Asp	Tyr	Val	Thr	Val 45
Arg	Lys	Asp	Ala	Tyr 50	Met	Phe	Trp	Trp	Leu 55	Tyr	Tyr	Ala	Thr	Asn 60
Ser	Суѕ	Lys	Asn	Phe 65	Ser	Glu	Leu	Pro	Leu 70	Val	Met	Trp	Leu	Gln 75
Gly	Gly	Pro	Gly	Gly 80	Ser	Ser	Thr	Gly	Phe 85	Gly	Asn	Phe	Glu	Glu 90
Ile	Gly	Pro	Leu	Asp 95	Ser	Asp	Leu	Lys	Pro 100	Arg	Lys	Thr	Thr	Trp 105
Leu	Gln	Ala	Ala	Ser 110	Leu	Leu	Phe	Val	Asp 115	Asn	Pro	Val	Gly	Thr 120
Gly	Phe	Ser	Tyr	Val 125	Asn	Gly	Ser	Gly	Ala 130	Tyr	Ala	Lys	Asp	Leu 135
Ala	Met	Val	Ala	Ser 140	Asp	Met	Met	Val	Leu 145	Leu	Lys	Thr	Phe	Phe 150
Ser	Cys	His	Lys	Glu 155	Phe	Gln	Thr	Val	Pro 160	Phe	Tyr	Ile	Phe	Ser 165
Glu	Ser	Tyr	Gly	Gly 170	Lys	Met	Ala	Ala	Gly 175	Ile	Gly	Leu	Glu	Leu 180
Tyr	Lys	Ala	Ile	Gln 185	Arg	Gly	Thr	Ile	Lys 190	Cys	Asn	Phe	Ala	Gly 195
Val	Ala	Leu	Gly	Asp 200	Ser	Trp	Ile	Ser	Pro 205	Val	Asp	Ser	Val	Leu 210
Ser	Trp	Gly	Pro	Tyr 215	Leu	Tyr	Ser	Met	Ser 220	Leu	Leu	Glu	Asp	Lys 225
Gly	Leu	Ala	Glu	Val 230	Ser	Lys	Val	Ala	Glu 235	Gln	Val	Leu	Asn	Ala 240

Val	Asn	Lys	Gly	Leu 245	Tyr	Arg	Glu	Ala	Thr 250	Glu	Leu	Trp	Gly	Lys 255
Ala	Glu	Met	Ile	Ile 260	Glu	Gln	Asn	Thr	Asp 265	Gly	Val	Asn	Phe	Tyr 270
Asn	Ile	Leu	Thr	Lys 275	Ser	Thr	Pro	Thr	Ser 280	Thr	Met	Glu	Ser	Ser 285
Leu	Glu	Phe	Thr	Gln 290	Ser	His	Leu	Val	Cys 295	Leu	Суѕ	Gln	Arg	His 300
Val	Arg	His	Leu	Gln 305	Arg	Asp	Ala	Leu	Ser 310	Gln	Leu	Met	Asn	Gly 315
Pro	Ile	Arg	Lys	Lys 320	Leu	Lys	Ile	Ile	Pro 325	Glu	Asp	Gln	Ser	Trp 330
Gly	Gly	Gln	Ala	Thr 335	Asn	Val	Phe	Val	Asn 340	Met	Glu	Glu	Asp	Phe 345
Met	Lys	Pro	Val	Ile 350	Ser	Ile	Val	Asp	Glu 355	Leu	Leu	Glu	Ala	Gly 360
Ile	Asn	Val	Thr	Val 365	Tyr	Asn	Gly	Gln	Leu 370	Asp	Leu	Ile	Val	Asp 375
Thr	Met	Gly	Gln	Glu 380	Ala	Trp	Val	Arg	Lys 385	Leu	Lys	Trp	Pro	Glu 390
Leu	Pro	Lys	Phe	Ser 395	Gln	Leu	Lys	Trp	Lys 400	Ala	Leu	Tyr	Ser	Asp 405
Pro	Lys	Ser	Leu	Glu 410	Thr	Ser	Ala	Phe	Val 415	Lys	Ser	Tyr	Lys	Asn 420
Leu	Ala	Phe	Tyr	Trp 425	Ile	Leu	Lys	Ala	Gly 430	His	Met	Val	Pro	Ser 435
Asp	Gln	Gly	Asp	Met 440	Ala	Leu	Lys	Met	Met 445	Arg	Leu	Val	Thr	Gln 450

Gln Glu

<210> 256

<211> 1100

<212> DNA

<213> Homo Sapien

<400> 256

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ccgttatcag gaccatgcgg ccgacgggtc atcacgtcgc gcatcgtggg 150
tggagaggac gccgaactcg ggcgttggcc gtggcagggg agcctgcgcc 200

tgtgggattc ccacgtatgc ggagtgagcc tgctcagcca ccgctgggca 250 ctcacggcgg cgcactgctt tgaaacctat agtgacctta gtgatccctc 300 cgggtggatg gtccagtttg gccagctgac ttccatgcca tccttctgga 350 geetgeagge etactacace egttactteg tategaatat etatetgage 400 cctcgctacc tggggaattc accctatgac attgccttgg tgaagctgtc 450 tgcacctgtc acctacacta aacacatcca gcccatctgt ctccaggcct 500 ccacatttga gtttgagaac cggacagact gctgggtgac tggctggggg 550 tacatcaaag aggatgaggc actgccatct ccccacaccc tccaggaagt 600 tcaggtcgcc atcataaaca actctatgtg caaccacctc ttcctcaagt 650 acagtttccg caaggacatc tttggagaca tggtttgtgc tggcaacgcc 700 caaggeggga aggatgeetg etteggtgae teaggtggae eettggeetg 750 taacaagaat ggactgtggt atcagattgg agtcgtgagc tggggagtgg 800 gctgtggtcg gcccaatcgg cccggtgtct acaccaatat cagccaccac 850 tttgagtgga tccagaagct gatggcccag agtggcatgt cccagccaga 900 cccctcctgg ccactactct ttttccctct tctctgggct ctcccactcc 950 tggggccggt ctgagcctac ctgagcccat gcagcctggg gccactgcca 1000 agtcaggccc tggttctctt ctgtcttgtt tggtaataaa cacattccag 1050 ttgatgcctt gcagggcatt cttcaaaaaa aaaaaaaaa aaaaaaaaa 1100

<210> 257

<211> 314

<212> PRT

<213> Homo Sapien

<400> 257

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Ala Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser

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Gly Pro Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly 35 40 45

Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg
50 55 60

Leu Trp Asp Ser His Val Cys Gly Val Ser Leu Leu Ser His Arg

80 85 90

Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu Thr Ser 95 100 105

Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr Phe 110 115 120

Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro 125 130 135

Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr
140 145 150

Lys His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe 155 160 165

Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys 170 175 180

Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln 185 190 195

Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys 200 205 210

Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala Gly 215 220 225

Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly 230 235 240

Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val 245 250 255

Val Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val 260 265 270

Tyr Thr Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met 275 280 285

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Phe Phe Pro Leu Leu Trp Ala Leu Pro Leu Leu Gly Pro Val 305

<210> 258

<211> 2427

<212> DNA

<213> Homo Sapien

<400> 258

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<210> 259

<211> 556

<212> PRT

<213> Homo Sapien

<400> 259

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Leu Pro Pro Gly Trp Val Ser Leu Gly Arg Ala Asp Pro Glu Glu
35 40 45

Glu Leu Ser Leu Thr Phe Ala Leu Arg Gln Gln Asn Val Glu Arg
50 55 60

Leu Ser	Glu I	Leu	Val 65	Gln	Ala	Val	Ser	Asp 70	Pro	Ser	Ser	Pro	Gln 75
Tyr Gly	Lys '	Tyr	Leu 80	Thr	Leu	Glu	Asn	Val 85	Ala	Asp	Leu	Val	Arg 90
Pro Ser	Pro 1	Leu	Thr 95	Leu	His	Thr	Val	Gln 100	Lys	Trp	Leu	Leu	Ala 105
Ala Gly	Ala	Gln	Lys 110	Cys	His	Ser	Val	Ile 115	Thr	Gln	Asp	Phe	Leu 120
Thr Cys	Trp 1	Leu	Ser 125	Ile	Arg	Gln	Ala	Glu 130	Leu	Leu	Leu	Pro	Gly 135
Ala Glu	Phe 1	His	His 140	Tyr	Val	Gly	Gly	Pro 145	Thr	Glu	Thr	His	Val 150
Val Arg	Ser 1	Pro	His 155	Pro	Tyr	Gln	Leu	Pro 160	Gln	Ala	Leu	Ala	Pro 165
His Val	Asp 1	Phe	Val 170	Gly	Gly	Leu	His	Arg 175	Phe	Pro	Pro	Thr	Ser 180
Ser Leu	Arg	Gln	Arg 185	Pro	Glu	Pro	Gln	Val 190	Thr	Gly	Thr	Val	Gly 195
Leu His	Leu (	Gly	Val 200	Thr	Pro	Ser	Val	Ile 205	Arg	Lys	Arg	Tyr	Asn 210
Leu Thr	Ser (	Gln	Asp 215	Val	Gly	Ser	Gly	Thr 220	Ser	Asn	Asn	Ser	Gln 225
Ala Cys	Ala	Gln	Phe 230	Leu	Glu	Gln	Tyr	Phe 235	His	Asp	Ser	Asp	Leu 240
Ala Gln	Phe I	Met	Arg 245	Leu	Phe	Gly	Gly	Asn 250	Phe	Ala	His	Gln	Ala 255
Ser Val	Ala	Arg	Val 260	Val	Gly	Gln	Gln	Gly 265	Arg	Gly	Arg	Ala	Gly 270
Ile Glu	Ala :	Ser	Leu 275	Asp	Val	Gln	Tyr	Leu 280	Met	Ser	Ala	Gly	Ala 285
Asn Ile	Ser '	Thr	Trp 290	Val	Tyr	Ser	Ser	Pro 295	Gly	Arg	His	Glu	Gly 300
Gln Glu	Pro 1	Phe	Leu 305	Gln	Trp	Leu	Met	Leu 310	Leu	Ser	Asn	Glu	Ser 315
Ala Leu	Pro 1	His	Val 320	His	Thr	Val	Ser	Tyr 325	Gly	Asp	Asp	Glu	Asp 330
Ser Leu	Ser :	Ser	Ala 335	Tyr	Ile	Gln	Arg	Val 340	Asn	Thr	Glu	Leu	Met 345

Lys	Ala	Ala	Ala	Arg 350	Gly	Leu	Thr	Leu	Leu 355	Phe	Ala	Ser	Gly	Asp 360
Ser	Gly	Ala	Gly	Cys 365	Trp	Ser	Val	Ser	Gly 370	Arg	His	Gln	Phe	Arg 375
Pro	Thr	Phe	Pro	Ala 380	Ser	Ser	Pro	Tyr	Val 385	Thr	Thr	Val	Gly	Gly 390
Thr	Ser	Phe	Gln	Glu 395	Pro	Phe	Leu	Ile	Thr 400	Asn	Glu	Ile	Val	Asp 405
Tyr	Ile	Ser	Gly	Gly 410	Gly	Phe	Ser	Asn	Val 415	Phe	Pro	Arg	Pro	Ser 420
Tyr	Gln	Glu	Glu	Ala 425	Val	Thr	Lys	Phe	Leu 430	Ser	Ser	Ser	Pro	His 435
Leu	Pro	Pro	Ser	Ser 440	Tyr	Phe	Asn	Ala	Ser 445	Gly	Arg	Ala	Tyr	Pro 450
Asp	Val	Ala	Ala	Leu 455	Ser	Asp	Gly	Tyr	Trp 460	Val	Val	Ser	Asn	Arg 465
Val	Pro	Ile	Pro	Trp 470	Val	Ser	Gly	Thr	Ser 475	Ala	Ser	Thr	Pro	Val 480
Phe	Gly	Gly	Ile	Leu 485	Ser	Leu	Ile	Asn	Glu 490	His	Arg	Ile	Leu	Ser 495
Gly	Arg	Pro	.Pro	Leu 500	Gly	Phe	Leu	Asn	Pro 505	Arg	Leu	Tyr	Gln	Gln 510
His	Gly	Ala	Gly	Leu 515	Phe	Asp	Val	Thr	Arg 520	Gly	Cys	His	Glu	Ser 525
Cys	Leu	Asp	Glu	Glu 530	Val	Glu	Gly	Gln	Gly 535	Phe	Cys	Ser	Gly	Pro 540
Gly	Trp	Asp	Pro	Val 545	Thr	Gly	Trp	Gly	Thr 550	Pro	Thr	Ser	Gln	Leu 555
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Cys

<210> 260

<211> 1638

<212> DNA

<213> Homo Sapien

<400> 260

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agtgagccct tacagtgccc cctggaaacc cacttggcct gcataccgcc 200 tccctgtcgt cttgccccag tctaccctca atttagccaa gccagacttt 250 ggagccgaag ccaaattaga agtatcttct tcatgtggac cccagtgtca 300 taagggaact ccactgccca cttacgaaga ggccaagcaa tatctgtctt 350 atgaaacgct ctatgccaat ggcagccgca cagagacgca ggtgggcatc 400 tacatcctca gcagtagtgg agatggggcc caacaccgag actcagggtc 450 ttcaggaaag tctcgaagga agcggcagat ttatggctat gacagcaggt 500 tcagcatttt tgggaaggac ttcctgctca actacccttt ctcaacatca 550 gtgaagttat ccacgggctg caccggcacc ctggtggcag agaagcatgt 600 cctcacagct gcccactgca tacacgatgg aaaaacctat gtgaaaggaa 650 cccagaagct tcgagtgggc ttcctaaagc ccaagtttaa agatggtggt 700 cgaggggcca acgactccac ttcagccatg cccgagcaga tgaaatttca 750 gtggatccgg gtgaaacgca cccatgtgcc caagggttgg atcaagggca 800 atgccaatga catcggcatg gattatgatt atgccctcct ggaactcaaa 850 aagccccaca agagaaaatt tatgaagatt ggggtgagcc ctcctgctaa 900 gcagctgcca gggggcagaa ttcacttctc tggttatgac aatgaccgac 950 caggcaattt ggtgtatcgc ttctgtgacg tcaaagacga gacctatgac 1000 ttgctctacc agcaatgcga tgcccagcca ggggccagcg ggtctggggt 1050 ctatgtgagg atgtggaaga gacagcagca gaagtgggag cgaaaaatta 1100 ttggcatttt ttcagggcac cagtgggtgg acatgaatgg ttccccacag 1150 gatttcaacg tggctgtcag aatcactcct ctcaaatatg cccagatttg 1200 ctattggatt aaaggaaact acctggattg tagggagggg tgacacagtg 1250 ttccctcctg gcagcaatta agggtcttca tgttcttatt ttaggagagg 1300 ccaaattgtt ttttgtcatt ggcgtgcaca cgtgtgtgtg tgtgtgtgt 1350 tgtgtgtaag gtgtcttata atcttttacc tatttcttac aattgcaaga 1400 tgactggctt tactatttga aaactggttt gtgtatcata tcatatatca 1450 tttaagcagt ttgaaggcat acttttgcat agaaataaaa aaaatactga 1500 tttggggcaa tgaggaatat ttgacaatta agttaatctt cacgtttttg 1550 caaactttga tttttatttc atctgaactt gtttcaaaga tttatattaa 1600

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<210> 261

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Thr	Trp	Pro	Ala	Tyr 35	Arg	Leu	Pro	Val	Val 40	Leu	Pro	Gln	Ser	Thr 45
Leu	Asn	Leu	Ala	Lys 50	Pro	Asp	Phe	Gly	Ala 55	Glu	Ala	Lys	Leu	Glu 60
Val	Ser	Ser	Ser	Cys 65	Gly	Pro	Gln	Cys	His 70	Lys	Gly	Thr	Pro	Leu 75
Pro	Thr	Tyr	Glu	Glu 80	Ala	Lys	Gln	Tyr	Leu 85	Ser	Tyr	Glu	Thr	Leu 90
Tyr	Ala	Asn	Gly	Ser	Arg	Thr	Glu	Thr	Gln	Val	Gly	Ile	Tyr	Ile
				95					100					105
Leu	Ser	Ser	Ser	Gly 110	Asp	Gly	Ala	Gln	His 115	Arg	Asp	Ser	Gly	Ser 120
Ser	Gly	Lys	Ser	Arg 125	Arg	Lys	Arg	Gln	Ile 130	Tyr	Gly	Tyr	Asp	Ser 135
Arg	Phe	Ser	Ile	Phe 140	Gly	Lys	Asp	Phe	Leu 145	Leu	Asn	Tyr	Pro	Phe 150
Ser	Thr	Ser	Val	Lys 155	Leu	Ser	Thr	Gly	Cys 160	Thr	Gly	Thr	Leu	Val 165
Ala	Glu	Lys	His	Val 170	Leu	Thr	Ala	Ala	His 175	Cys	Ile	His	Asp	Gly 180
Lys	Thr	Tyr	Val	Lys 185	Gly	Thr	Gln	Lys	Leu 190	Arg	Val	Gly	Phe	Leu 195
Lys	Pro	Lys	Phe	Lys 200	Asp	Gly	Gly	Arg	Gly 205	Ala	Asn	Asp	Ser	Thr 210
Ser	Ala	Met	Pro	Glu 215	Gln	Met	Lys	Phe	Gln 220	Trp	Ile	Arg	Val	Lys 225
Arg	Thr	His	Val	Pro 230	Lys	Gly	Trp	Ile	Lys 235	Gly	Asn	Ala	Asn	Asp 240

Ile	Gly	Met	Asp	Tyr 245	Asp	Tyr	Ala	Leu	Leu 250	Glu	Leu	Lys	Lys	Pro 255
His	Lys	Arg	Lys	Phe 260	Met	Lys	Ile	Gly	Val 265	Ser	Pro	Pro	Ala	Lys 270
Gln	Leu	Pro	Gly	Gly 275	Arg	Ile	His	Phe	Ser 280	Gly	Tyr	Asp	Asn	Asp 285
Arg	Pro	Gly	Asn	Leu 290	Val	Tyr	Arg	Phe	Cys 295	Asp	Val	Lys	Asp	Glu 300
Thr	Tyr	Asp	Leu	Leu 305	Tyr	Gln	Gln	Cys	Asp 310	Ala	Gln	Pro	Gly	Ala 315
Ser	Gly	Ser	Gly	Val 320	Tyr	Val	Arg	Met	Trp 325	Lys	Arg	Gln	Gln	Gln 330
Lys	Trp	Glu	Arg	Lys 335	Ile	Ile	Gly	Ile	Phe 340	Ser	Gly	His	Gln	Trp 345
Val	Asp	Met	Asn	Gly 350	Ser	Pro	Gln	Asp	Phe 355	Asn	Val	Ala	Val	Arg 360
Ile	Thr	Pro	Leu	Lys 365	Tyr	Ala	Gln	Ile	Cys 370	Tyr	Trp	Ile	Lys	Gly 375
Asn	Tyr	Leu	Asp	Cys 380	Arg	Glu	Gly							

<210> 262

<211> 1378

<212> DNA

<213> Homo Sapien

<400> 262

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acetteacet ccetgetget getggegteg acagecatec teaatgegge 150
caggatacet gtteececag cetgtgggaa geeceageag etgaaceggg 200
ttgtgggggg egaggacage actgacageg agtggeetg gategtgage 250
atecagaaga atgggacea ecaetgegea ggttetetge teaecageeg 300
ctgggtgate actgetgee actgtteaa ggacaacetg aacaaaceat 350
acetgttete tgtgetget ggggeetgge agetgggaa ecetggetet 400
cggteecaga aggtggtgt tgeetggtg gageeceaee etgtgate 450
ctggaaggaa ggtgeetgtg cagacattge ectggtget etegagege 500

ccatacagtt ctcagagcgg gtcctgccca tctgcctacc tgatgcctct 550 atccacctcc ctccaaacac ccactgctgg atctcaggct gggggagcat 600 ccaagatgga gttcccttgc cccaccctca gaccctgcag aagctgaagg 650 ttcctatcat cgactcggaa gtctgcagcc atctgtactg gcggggagca 700 ggacagggac ccatcactga ggacatgctg tgtgccggct acttggaggg 750 ggagcgggat gcttgtctgg gcgactccgg gggccccctc atgtgccagg 800 tggacggcgc ctggctgctg gccggcatca tcagctgggg cgagggctgt 850 gccgagcgca acaggcccgg ggtctacatc agcctctctg cgcaccqctc 900 ctgggtggag aagatcgtgc aaggggtgca gctccgcggg cgcgctcagg 950 ggggtgggc cctcagggca ccgagccagg gctctggggc cgccgcgcgc 1000 tcctagggcg cagcgggacg cgggctcgg atctgaaagg cggccagatc 1050 cacatetgga tetggatetg eggeggeete gggeggttte eeeegeegta 1100 aataggetea tetaceteta eetetggggg eeeggaegge tgetgeggaa 1150 aggaaacccc ctccccgacc cgcccgacgg cctcaqgccc ccctccaagg 1200 catcaggeec egeceaacgg ceteatgtee eegeceecac gaetteegge 1250 cccqccccq qqccccaqcq cttttqtqta tataaatqtt aatqattttt 1300 ataggtattt gtaaccctgc ccacatatct tatttattcc tccaatttca 1350 ataaattatt tattctccaa aaaaaaaa 1378

<210> 263

<211> 317

<212> PRT

<213> Homo Sapien

<400> 263

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Gly Thr Phe Thr Ser Leu Leu Leu Leu Ala Ser Thr Ala Ile Leu 20 25 30

Asn Ala Ala Arg Ile Pro Val Pro Pro Ala Cys Gly Lys Pro Gln
35 40 45

Gln Leu Asn Arg Val Val Gly Gly Glu Asp Ser Thr Asp Ser Glu  $50 \,\,$  55  $\,\,$  60

Trp Pro Trp Ile Val Ser Ile Gln Lys Asn Gly Thr His His Cys
65 70 75

Ala	Gly	Ser	Leu	Leu 80	Thr	Ser	Arg	Trp	Val 85	Ile	Thr	Ala	Ala	His 90
Cys	Phe	Lys	Asp	Asn 95	Leu	Asn	Lys	Pro	Tyr 100	Leu	Phe	Ser	Val	Leu 105
Leu	Gly	Ala	Trp	Gln 110	Leu	Gly	Asn	Pro	Gly 115	Ser	Arg	Ser	Gln	Lys 120
Val	Gly	Val	Ala	Trp 125	Val	Glu	Pro	His	Pro 130	Val	Tyr	Ser	Trp	Lys 135
Glu	Gly	Ala	Cys	Ala 140	Asp	Ile	Ala	Leu	Val 145	Arg	Leu	Glu	Arg	Ser 150
Ile	Gln	Phe	Ser	Glu 155	Arg	Val	Leu	Pro	Ile 160	Cys	Leu	Pro	Asp	Ala 165
Ser	Ile	His	Leu	Pro 170	Pro	Asn	Thr	His	Cys 175	Trp	Ile	Ser	Gly	Trp 180
Gly	Ser	Ile	Gln	Asp 185	Gly	Val	Pro	Leu	Pro 190	His	Pro	Gln	Thr	Leu 195
Gln	Lys	Leu	Lys	Val 200	Pro	Ile	Ile	Asp	Ser 205	Glu	Val	Cys	Ser	His 210
Leu	Tyr	Trp	Arg	Gly 215	Ala	Gly	Gln	Gly	Pro 220	Ile	Thr	Glu	Asp	Met 225
Leu	Cys	Ala	Gly	Tyr 230	Leu	Glu	Gly	Glu	Arg 235	Asp	Ala	Cys	Leu	Gly 240
Asp	Ser	Gly	Gly	Pro 245	Leu	Met	Cys	Gln	Val 250	Asp	Gly	Ala	Trp	Leu 255
Leu	Ala	Gly	Ile	Ile 260	Ser	Trp	Gly	Glu	Gly 265	Cys	Ala	Glu	Arg	Asn 270
Arg	Pro	Gly	Val	Tyr 275	Ile	Ser	Leu	Ser	Ala 280	His	Arg	Ser	Trp	Val 285
Glu	Lys	Ile	Val	Gln 290	Gly	Val	Gln	Leu	Arg 295	Gly	Arg	Ala	Gln	Gly 300
Gly	Gly	Ala	Leu	Arg 305	Ala	Pro	Ser	Gln	Gly 310	Ser	Gly	Ala	Ala	Ala 315

Arg Ser

<210> 264 <211> 24

<212> DNA

<213> Artificial Sequence

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 <400> 264
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<400> 265
 gcagaggtgt ctaaggttg 19
<210> 266
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 266
 agetetagae caatgecage ttee 24
<210> 267
<211> 45
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 267
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<210> 268
<211> 25
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 268
ggggaattca ccctatgaca ttgcc 25
<210> 269
<211> 24
<212> DNA
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<223> Synthetic Oligonucleotide Probe
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<400> 269
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<210> 270
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<223> Synthetic Oligonucleotide Probe
<400> 270
 gcacctgtca cctacactaa acacatccag cccatctgtc tccaggcctc 50
<210> 271
<211> 26
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 271
 gcggaagggc agaatgggac tccaag 26
<210> 272
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 272
 cagccctgcc acatgtgc 18
<210> 273
<211> 18
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 273
 tactgggtgg tcagcaac 18
<210> 274
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 274
 ggcgaagagc agggtgagac cccg 24
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<211> 45
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<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
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<210> 276
<211> 21
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
<400> 276
 gggcagggat tccagggctc c 21
<210> 277
<211> 18
<212> DNA
<213> Artificial Sequence
<223> Synthetic Oligonucleotide Probe
<400> 277
 ggctatgaca gcaggttc 18
<210> 278
<211> 18
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 278
tgacaatgac cgaccagg 18
<210> 279
<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 279
 gcatcgcatt gctggtagag caag 24
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<210> 281
<211> 34
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 cgtctcgagc gctccataca gttcccttgc ccca 34
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<212> DNA
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<400> 282
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tgccaggtgg a 61
<210> 283
<211> 119
<212> DNA
<213> Artificial Sequence
<220>
<223> Synthetic Oligonucleotide Probe
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gcagccatct gtactggcgg ggagcaggac agggacccat cactgaggac 100
atgctgtgtg ccggctact 119
<210> 284
<211> 1875
<212> DNA
<213> Homo Sapien
<400> 284
gacggctggc caccatgcac ggctcctgca gtttcctgat gcttctgctg 50
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ccgctactgc tactgctggt ggccaccaca ggccccgttg gagccctcac 100 agatgaggag aaacgtttga tggtggagct gcacaacctc taccgggccc 150 aggtatecee gaeggeetea gaeatgetge acatgagatg ggaegaggag 200 ctggccgcct tcgccaaggc ctacgcacgg cagtgcgtgt ggggccacaa 250 caaggagege gggegeegeg gegagaatet gttegeeate acagaegagg 300 gcatggacgt gccgctggcc atggaggagt ggcaccacga gcgtgagcac 350 tacaacctca gcgccgccac ctgcagccca ggccagatgt gcggccacta 400 cacgcaggtg gtatgggcca agacagagag gatcggctgt ggttcccact 450 tctgtgagaa gctccagggt gttgaggaga ccaacatcga attactggtg 500 tgcaactatg agcctccggg gaacgtgaag gggaaacggc cctaccagga 550 ggggacteeg tgeteceaat gteeetetgg etaccaetge aagaacteee 600 tctgtgaacc catcggaagc ccggaagatg ctcaggattt gccttacctg 650 gtaactgagg ccccatcctt ccgggcgact gaagcatcag actctaggaa 700 aatgggtact cettetteee tageaacggg gatteegget ttettggtaa 750 cagaggtete aggeteeetg geaaceaagg etetgeetge tgtggaaace 800 caggececaa etteettage aacgaaagae eegeeeteea tggeaacaga 850 ggctccacct tgcgtaacaa ctgaggtccc ttccattttg gcagctcaca 900 gcctgccctc cttggatgag gagccagtta ccttccccaa atcgacccat 950 gttcctatcc caaaatcagc agacaaagtg acagacaaaa caaaagtgcc 1000 ctctaggagc ccagagaact ctctggaccc caagatgtcc ctgacagggg 1050 caagggaact cctaccccat gcccaggagg aggctgaggc tgaggctgag 1100 ttgcctcctt ccagtgaggt cttggcctca gtttttccag cccaggacaa 1150 gccaggtgag ctgcaggcca cactggacca cacggggcac acctcctcca 1200 agtccctgcc caatttcccc aatacctctg ccaccgctaa tgccacgggt 1250 gggcgtgccc tggctctgca gtcgtccttg ccaggtgcag agggccctga 1300 caagectage gttgtgtcag ggetgaacte gggeeetggt catgtgtggg 1350 gccctctcct gggactactg ctcctgcctc ctctggtgtt ggctggaatc 1400 ttctgaatgg gataccactc aaagggtgaa gaggtcagct gtcctcctgt 1450

catcttcccc accetytecc cagecectaa acaagatact tettggttaa 1500 ggccctccgg aagggaaagg etacggggca tgtgeeteat cacaceatee 1550 ateetggagg cacaaggeet ggetggetge gageteagga ggeegeetga 1600 ggaetgeaca eegggeeeac aceteteetg eeeeteeete etgagteetg 1650 ggggtgggag gatttgaggg ageteactge etacetggee tggggetgte 1700 tgeecacaca geatgtgege tetecetgag tgeetgtta getggggatg 1750 gggatteeta ggggeagatg aaggaeaage eeeactggag tggggttett 1800 tgagtgggg aggeaggae gagggaagga aagtaaetee tgaeteteea 1850 ataaaaacet gteeaacetg tgaaa 1875

<210> 285

<211> 463

<212> PRT

<213> Homo Sapien

<400> 285

Met His Gly Ser Cys Ser Phe Leu Met Leu Leu Leu Pro Leu Leu 1 5 10 15

Leu Leu Leu Val Ala Thr Thr Gly Pro Val Gly Ala Leu Thr Asp 20 25 30

Glu Glu Lys Arg Leu Met Val Glu Leu His Asn Leu Tyr Arg Ala 35 40 45

Gln Val Ser Pro Thr Ala Ser Asp Met Leu His Met Arg Trp Asp
50 55 60

Glu Glu Leu Ala Ala Phe Ala Lys Ala Tyr Ala Arg Gln Cys Val 65 70 75

Trp Gly His Asn Lys Glu Arg Gly Arg Gly Glu Asn Leu Phe 80 85 90

Ala Ile Thr Asp Glu Gly Met Asp Val Pro Leu Ala Met Glu Glu 95 100 105

Trp His His Glu Arg Glu His Tyr Asn Leu Ser Ala Ala Thr Cys 110 115 120

Ser Pro Gly Gln Met Cys Gly His Tyr Thr Gln Val Val Trp Ala 125 130 135

Lys Thr Glu Arg Ile Gly Cys Gly Ser His Phe Cys Glu Lys Leu 140 145 150

Gln Gly Val Glu Glu Thr Asn Ile Glu Leu Leu Val Cys Asn Tyr 155 160 165

Glu	Pro	Pro	Gly	Asn 170	Val	Lys	Gly	Lys	Arg 175	Pro	Tyr	Gln	Glu	Gly 180
Thr	Pro	Cys	Ser	Gln 185	Cys	Pro	Ser	Gly	Tyr 190	His	Суѕ	Lys	Asn	Ser 195
Leu	Cys	Glu	Pro	Ile 200	Gly	Ser	Pro	Glu	Asp 205	Ala	Gln	Asp	Leu	Pro 210
Tyr	Leu	Val	Thr	Glu 215	Ala	Pro	Ser	Phe	Arg 220	Ala	Thr	Glu	Ala	Ser 225
Asp	Ser	Arg	Lys	Met 230	Gly	Thr	Pro	Ser	Ser 235	Leu	Ala	Thr	Gly	Ile 240
Pro	Ala	Phe	Leu	Val 245	Thr	Glu	Val	Ser	Gly 250	Ser	Leu	Ala	Thr	Lys 255
Ala	Leu	Pro	Ala	Val 260	Glu	Thr	Gln	Ala	Pro 265	Thr	Ser	Leu	Ala	Thr 270
Lys	Asp	Pro	Pro	Ser 275	Met	Ala	Thr	Glu	Ala 280	Pro	Pro	Cys	Val	Thr 285
Thr	Glu	Val	Pro	Ser 290	Ile	Leu	Ala	Ala	His 295	Ser	Leu	Pro	Ser	Leu 300
Asp	Glu	Glu	Pro	Val 305	Thr	Phe	Pro	Lys	Ser 310	Thr	His	Val	Pro	Ile 315
Pro	Lys	Ser	Ala	Asp 320	Lys	Val	Thr	Asp	Lys 325	Thr	Lys	Val	Pro	Ser 330
Arg	Ser	Pro	Glu	Asn 335	Ser	Leu	Asp	Pro	Lys 340	Met	Ser	Leu	Thr	Gly 345
Ala	Arg	Glu	Leu	Leu 350	Pro	His	Ala	Gln	Glu 355	Glu	Ala	Glu	Ala	Glu 360
Ala	Glu	Leu	Pro	Pro 365	Ser	Ser	Glu	Val	Leu 370	Ala	Ser	Val	Phe	Pro 375
Ala	Gln	Asp	Lys	Pro 380	Gly	Glu	Leu	Gln	Ala 385	Thr	Leu	Asp	His	Thr 390
Gly	His	Thr	Ser	Ser 395	Lys	Ser	Leu	Pro	Asn 400	Phe	Pro	Asn	Thr	Ser 405
Ala	Thr	Ala	Asn	Ala 410	Thr	Gly	Gly	Arg	Ala 415	Leu	Ala	Leu	Gln	Ser 420
Ser	Leu	Pro	Gly	Ala 425	Glu	Gly	Pro	Asp	Lys 430	Pro	Ser	Val	Val	Ser 435
Gly	Leu	Asn	Ser	Gly 440	Pro	Gly	His	Val	Trp 445	Gly	Pro	Leu	Leu	Gly 450

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<400> 286
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<211> 24
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 287
ctcatattgc acaccagtaa ttcg 24
<210> 288
<211> 45
<212> DNA
<213> Artificial Sequence
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<223> Synthetic Oligonucleotide Probe
<400> 288
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<212> DNA
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 caaggcaagt tccatgagcc accttcaaag ccttcgagaa gtgaaactga 200
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 attacacttc tctccttggc tggaaacagg attgttgaaa tactccctga 300
 acatetgaaa gagttteagt eeettgaaac tttggaeett ageageaaca 350
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atatttcaga gctccaaact gcatttccag ccctacagct caaatatctg 400

Leu Leu Leu Pro Pro Leu Val Leu Ala Gly Ile Phe

tatctcaaca gcaaccgagt cacatcaatg gaacctgggt attttgacaa 450 tttggccaac acactccttg tgttaaagct gaacaggaac cgaatctcag 500 ctatcccacc caagatgttt aaactgcccc aactgcaaca tctcgaattg 550 aaccgaaaca agattaaaaa tgtagatgga ctgacattcc aaggccttgg 600 tgctctgaag tctctgaaaa tgcaaagaaa tggagtaacg aaacttatgg 650 atggagcttt ttgggggctg agcaacatgg aaattttgca gctggaccat 700 aacaacctaa cagagattac caaaggctgg ctttacggct tgctgatgct 750 gcaggaactt catctcagcc aaaatgccat caacaggatc agccctgatg 800 cctgggagtt ctgccagaag ctcagtgagc tggacctaac tttcaatcac 850 ttatcaaggt tagatgattc aagcttcctt ggcctaagct tactaaatac 900 actgcacatt gggaacaaca gagtcagcta cattgctgat tgtgccttcc 950 gggggctttc cagtttaaag actttggatc tgaagaacaa tgaaatttcc 1000 tggactattg aagacatgaa tggtgctttc tctgggcttg acaaactgag 1050 gcgactgata ctccaaggaa atcggatccg ttctattact aaaaaagcct 1100 tcactggttt ggatgcattg gagcatctag acctgagtga caacgcaatc 1150 atgtetttae aaggeaatge atttteacaa atgaagaaac tgeaacaatt 1200 gcatttaaat acatcaagcc ttttgtgcga ttgccagcta aaatggctcc 1250 cacagtgggt ggcggaaaac aactttcaga gctttgtaaa tgccagttgt 1300 gcccatcctc agctgctaaa aggaagaagc atttttgctg ttagcccaga 1350 tggctttgtg tgtgatgatt ttcccaaacc ccagatcacg gttcagccag 1400 aaacacagtc ggcaataaaa ggttccaatt tgagtttcat ctgctcagct 1450 gccagcagca gtgattcccc aatgactttt gcttggaaaa aagacaatga 1500 actactgcat gatgctgaaa tggaaaatta tgcacacctc cgggcccaag 1550 gtggcgaggt gatggagtat accaccatcc ttcggctgcg cgaggtggaa 1600 tttgccagtg aggggaaata tcagtgtgtc atctccaatc actttggttc 1650 atcctactct gtcaaagcca agcttacagt aaatatgctt ccctcattca 1700 ccaagacccc catggatctc accatccgag ctggggccat ggcacgcttg 1750 gagtgtgctg ctgtggggca cccagccccc cagatagcct ggcagaagga 1800

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tgagaccaaa ggaaaagctt aacatactac ctcaagtgaa cttttattta 3300 aaagagagag aatcttatgt tttttaaatg gagttatgaa ttttaaaagg 3350 ataaaaatgc tttattata cagatgaacc aaaattacaa aaagttatga 3400 aaatttttat actgggaatg atgctcatat aagaatacct ttttaaacta 3450 ttttttaact ttgttttatg caaaaaagta tcttacgtaa attaatgata 3500 taaatcatga ttatttatg tattttata atgccagatt tcttttatg 3550 gaaaatgagt tactaaagca ttttaaataa tacctgcctt gtaccattt 3600 ttaaaatagaa gttacttcat tatattttgc acattatatt taataaaatg 3650 tgtcaatttg aa 3662

<210> 290

<211> 1059

<212> PRT

<213> Homo Sapien

<400> 290

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20 25 30

Ala Ser Ser Met Ser His Leu Gln Ser Leu Arg Glu Val Lys Leu 35 40 45

Asn Asn Glu Leu Glu Thr Ile Pro Asn Leu Gly Pro Val Ser
50 55 60

Ala Asn Ile Thr Leu Leu Ser Leu Ala Gly Asn Arg Ile Val Glu
65 70 75

Ile Leu Pro Glu His Leu Lys Glu Phe Gln Ser Leu Glu Thr Leu 80 85 90

Asp Leu Ser Ser Asn Asn Ile Ser Glu Leu Gln Thr Ala Phe Pro 95 100 105

Ala Leu Gln Leu Lys Tyr Leu Tyr Leu Asn Ser Asn Arg Val Thr 110 115 120

Ser Met Glu Pro Gly Tyr Phe Asp Asn Leu Ala Asn Thr Leu Leu 125 130 135

Val Leu Lys Leu Asn Arg Asn Arg Ile Ser Ala Ile Pro Pro Lys 140 145 150

Met Phe Lys Leu Pro Gln Leu Gln His Leu Glu Leu Asn Arg Asn

Phe Thr Gly Leu Asp Ala Leu Glu His Leu Asp Leu Ser Asp Asn 360

Ala Ile Met Ser Leu Gln Gly Asn Ala Phe Ser Gln Met Lys Lys 375

Leu Gln Gln Leu His Jao Phe Asn Thr Ser Ser Leu Leu Cys Asp Cys 380

Gln Leu Lys Trp Leu Pro Gln Trp Val Ala Glu Asn Asn Phe Gln 405

Ser Phe Val Asn Ala Ser Cys Ala His Pro Gln Leu Leu Lys Gly 420

Arg Ser Ile Phe Ala Val Ser Pro Asp Gly Phe Val Cys Asp Asp Asp Asp Phe Pro Lys Pro Gln Ile Thr Val Gln Pro Glu Thr Gln Ser Ala

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S	er	Asp	Ser	Pro	Met	Thr	Phe	Ala	Trp	Lys	Lys	Asp	Asn	Glu	Leu
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L	eu	His	Asp	Ala	Glu 485	Met	Glu	Asn	Tyr	Ala 490	His	Leu	Arg	Ala	Gln 495
G.	ly	Gly	Glu	Val	Met 500	Glu	Tyr	Thr	Thr	Ile 505	Leu	Arg	Leu	Arg	Glu 510
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A.	la	Gly	Ala	Met	Ala 560	Arg	Leu	Glu	Cys	Ala 565	Ala	Val	Gly	His	Pro 570
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A	la	Ala	Arg	Glu	Arg 590	Arg	Met	His	Val	Met 595	Pro	Glu	Asp	Asp	Val 600
Pl	he	Phe	Ile	Val	Asp 605	Val	Lys	Ile	Glu	Asp 610	Ile	Gly	Val	Tyr	Ser 615
C	ys	Thr	Ala	Gln	Asn 620	Ser	Ala	Gly	Ser	Ile 625	Ser	Ala	Asn	Ala	Thr 630
L	eu	Thr	Val	Leu	Glu 635	Thr	Pro	Ser	Phe	Leu 640	Arg	Pro	Leu	Leu	Asp 645
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P	ro	Leu	Val	Val	Thr 680	Glu	Arg	His	Phe	Phe 685	Ala	Ala	Gly	Asn	Gln 690
L	eu	Leu	Ile	Ile	Val 695	Asp	Ser	Asp	Val	Ser 700	Asp	Ala	Gly	Lys	Tyr 705
T	hr	Cys	Glu	Met	Ser 710	Asn	Thr	Leu	Gly	Thr 715	Glu	Arg	Gly	Asn	Val 720

Arg	Leu	Ser	Val	Ile 725	Pro	Thr	Pro	Thr	Cys 730	Asp	Ser	Pro	Gln	Met 735
Thr	Ala	Pro	Ser	Leu 740	Asp	Asp	Asp	Gly	Trp 745	Ala	Thr	Val	Gly	Val 750
Val	Ile	Ile	Ala	Val 755	Val	Cys	Cys	Val	Val 760	Gly	Thr	Ser	Leu	Val 765
Trp	Val	Val	Ile	Ile 770	Tyr	His	Thr	Arg	Arg 775	Arg	Asn	Glu	Asp	Cys 780
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Ser	Tyr	Leu	Ser	Ser 800	Gln	Gly	Thr	Leu	Ala 805	Asp	Arg	Gln	Asp	Gly 810
Tyr	Val	Ser	Ser	Glu 815	Ser	Gly	Ser	His	His 820	Gln	Phe	Val	Thr	Ser 825
Ser	Gly	Ala	Gly	Phe 830	Phe	Leu	Pro	Gln	His 835	Asp	Ser	Ser	Gly	Thr 840
Cys	His	Ile	Asp	Asn 845	Ser	Ser	Glu	Ala	Asp 850	Val	Glu	Ala	Ala	Thr 855
Asp	Leu	Phe	Leu	Cys 860	Pro	Phe	Leu	Gly	Ser 865	Thr	Gly	Pro	Met	Tyr 870
Leu	Lys	Gly	Asn	Val 875	Tyr	Gly	Ser	Asp	Pro 880	Phe	Glu	Thr	Tyr	His 885
Thr	Gly	Cys	Ser	Pro 890	Asp	Pro	Arg	Thr	Val 895	Leu	Met	Asp	His	Tyr 900
Glu	Pro	Ser	Tyr	Ile 905	Lys	Lys	Lys	Glu	Cys 910	Tyr	Pro	Cys	Ser	His 915
Pro	Ser	Glu	Glu	Ser 920	Cys	Glu	Arg	Ser	Phe 925	Ser	Asn	Ile	Ser	Trp 930
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Glu	Gly	Pro	Gly	Met 950	Lys	Asn	Leu	Cys	Leu 955	Asn	Lys	Ser	Ser	Leu 960
Asp	Phe	Ser	Ala	Asn 965	Pro	Glu	Pro	Ala	Ser 970	Val	Ala	Ser	Ser	Asn 975
Ser	Phe	Met	Gly	Thr 980	Phe	Gly	Lys	Ala	Leu 985	Arg	Arg	Pro	His	Leu 990
Asp	Ala	Tyr	Ser	Ser 995	Phe	Gly	Gln		Ser .000	Asp	Cys	Gln		Arg .005

Ala Phe Tyr Leu Lys Ala His Ser Ser Pro Asp Leu Asp Ser Gly
1010 1015 1020

Ser Glu Glu Asp Gly Lys Glu Arg Thr Asp Phe Gln Glu Glu Asn 1025 1030 1035

His Ile Cys Thr Phe Lys Gln Thr Leu Glu Asn Tyr Arg Thr Pro  $1040 \hspace{1cm} 1045 \hspace{1cm} 1050$ 

Asn Phe Gln Ser Tyr Asp Leu Asp Thr 1055

<210> 291

<211> 2906

<212> DNA

<213> Homo Sapien

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<210> 292

<211> 640

<212> PRT

<213> Homo Sapien

<400> 292

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Leu Ala Leu Gl<br/>n Leu Leu Val Val Ala Gly Leu Val Arg Ala Gl<br/>n \$35\$ 40 45

Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
50 55 60

Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser 65 70 75

Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile 80 85 90

Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
95 100 105

Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe \$110\$ \$120\$

Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg 125 130 135

Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu

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Thr Ala Ser Ala	Thr Leu Asn 440	Val Thr Ala Ala 445	Thr Thr Thr Pr	
Phe Ser Tyr Phe	Ser Thr Val 455	Thr Val Glu Thr 460		er 55
Gln Asp Glu Ala	Arg Thr Thr 470	Asp Asn Asn Val 475	Gly Pro Thr Pr	
Val Val Asp Trp	Glu Thr Thr 485	Asn Val Thr Thr 490	Ser Leu Thr Pr	
Gln Ser Thr Arg	Ser Thr Glu 500	Lys Thr Phe Thr 505	Ile Pro Val Th	
Asp Ile Asn Ser	Gly Ile Pro 515	Gly Ile Asp Glu 520	Val Met Lys Th	
Thr Lys Ile Ile	Ile Gly Cys 530	Phe Val Ala Ile 535	Thr Leu Met Al	
Ala Val Met Leu	Val Ile Phe 545	Tyr Lys Met Arg 550	Lys Gln His Hi 55	
Arg Gln Asn His	His Ala Pro 560	Thr Arg Thr Val 565	Glu Ile Ile As	
Val Asp Asp Glu	Ile Thr Gly 575	Asp Thr Pro Met 580	Glu Ser His Le 58	
Pro Met Pro Ala	Ile Glu His 590	Glu His Leu Asn 595	His Tyr Asn Se	
Tyr Lys Ser Pro	Phe Asn His 605	Thr Thr Thr Val 610	Asn Thr Ile As	
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<211> 4053

<212> DNA

<213> Homo Sapien

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gagggcgggc gtgcaccctc ggctggaagt ttgtgccggg ccccgagcgc 200 gcgccggctg ggagcttcgg gtagagacct aggccgctgg accgcgatga 250 gcgcccgag cctccgtgcg cgcgccgcgg ggttggggct gctgctgtgc 300 gcggtgctgg ggcgcgctgg ccggtccgac agcggcggtc gcggggaact 350 cgggcagccc tctggggtag ccgccgagcg cccatgcccc actacctgcc 400 gctgcctcgg ggacctgctg gactgcagtc gtaagcggct agcgcgtctt 450 cccgagccac tcccgtcctg ggtcgctcgg ctggacttaa gtcacaacag 500 attatctttc atcaaggcaa gttccatgag ccaccttcaa agccttcgag 550 aagtgaaact gaacaacaat gaattggaga ccattccaaa tctgggacca 600 gtctcggcaa atattacact tctctccttg gctggaaaca ggattgttga 650 aatactccct gaacatctga aagagtttca gtcccttgaa actttggacc 700 ttagcagcaa caatatttca gagctccaaa ctgcatttcc agccctacag 750 ctcaaatatc tgtatctcaa cagcaaccga gtcacatcaa tggaacctgg 800 gtattttgac aatttggcca acacactcct tgtgttaaag ctgaacagga 850 accgaatctc agctatccca cccaagatgt ttaaactgcc ccaactgcaa 900 catctcgaat tgaaccgaaa caagattaaa aatgtagatg gactgacatt 950 ccaaggeett ggtgetetga agtetetgaa aatgeaaaga aatggagtaa 1000 cgaaacttat ggatggagct ttttgggggc tgagcaacat ggaaattttg 1050 cagctggacc ataacaacct aacagagatt accaaaggct ggctttacgg 1100 cttgctgatg ctgcaggaac ttcatctcag ccaaaatgcc atcaacagga 1150 tcagccctga tgcctgggag ttctgccaga agctcagtga gctggaccta 1200 actttcaatc acttatcaag gttagatgat tcaagcttcc ttggcctaag 1250 cttactaaat acactgcaca ttgggaacaa cagagtcagc tacattgctg 1300 attgtgcctt ccgggggctt tccagtttaa agactttgga tctgaagaac 1350 aatgaaattt cctggactat tgaagacatg aatggtgctt tctctgggct 1400 tgacaaactg aggcgactga tactccaagg aaatcggatc cgttctatta 1450 ctaaaaaagc cttcactggt ttggatgcat tggagcatct agacctgagt 1500 gacaacgcaa tcatgtcttt acaaggcaat gcattttcac aaatgaagaa 1550 actgcaacaa ttgcatttaa atacatcaag ccttttgtgc gattgccagc 1600

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<211> 1119

<212> PRT

<213> Homo Sapien

<400> 294

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Gly Arg Gly Glu Leu Gly Gln Pro Ser Gly Val Ala Ala Glu Arg

Pro	Cys	Pro	Thr	Thr 50	Cys	Arg	Суѕ	Leu	Gly 55	Asp	Leu	Leu	Asp	Cys 60
Ser	Arg	Lys	Arg	Leu 65	Ala	Arg	Leu	Pro	Glu 70	Pro	Leu	Pro	Ser	Trp 75
Val	Ala	Arg	Leu	Asp 80	Leu	Ser	His	Asn	Arg 85	Leu	Ser	Phe	Ile	Lys 90
Ala	Ser	Ser	Met	Ser 95	His	Leu	Gln	Ser	Leu 100	Arg	Glu	Val	Lys	Let 105
Asn	Asn	Asn	Glu	Leu 110	Glu	Thr	Ile	Pro	Asn 115	Leu	Gly	Pro	Val	Ser 120
Ala	Asn	Ile	Thr	Leu 125	Leu	Ser	Leu	Ala	Gly 130	Asn	Arg	Ile	Val	Glu 135
Ile	Leu	Pro	Glu	His 140	Leu	Lys	Glu	Phe	Gln 145	Ser	Leu	Glu	Thr	Le: 150
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Ala	Leu	Gln	Leu	Lys 170	Tyr	Leu	Tyr	Leu	Asn 175	Ser	Asn	Arg	Val	Th: 180
Ser	Met	Glu	Pro	Gly 185	Tyr	Phe	Asp	Asn	Leu 190	Ala	Asn	Thr	Leu	Let 195
Val	Leu	Lys	Leu	Asn 200	Arg	Asn	Arg	Ile	Ser 205	Ala	Ile	Pro	Pro	Lys 210
Met	Phe	Lys	Leu	Pro 215	Gln	Leu	Gln	His	Leu 220	Glu	Leu	Asn	Arg	Asr 225
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Asp	Gly	Ala	Phe	Trp 260	Gly	Leu	Ser	Asn	Met 265	Glu	Ile	Leu	Gln	Let 270
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				305		Trp			310					315
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Glu	Gly	Pro	Gly 1	Met .010	Lys	Asn	Leu		Leu 1015	Asn	Lys	Ser		Leu 020
Asp	Phe	Ser	Ala 1	Asn .025	Pro	Glu	Pro		Ser .030	Val	Ala	Ser		Asn 035
Ser	Phe	Met	Gly 1	Thr 040	Phe	Gly	Lys		Leu .045	Arg	Arg	Pro		Leu 050
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Ala	Phe	Tyr	Leu 1	Lys 070	Ala	His	Ser		Pro .075	Asp	Leu	Asp		Gly 080
Ser	Glu	Glu	Asp 1	Gly 085	Lys	Glu	Arg		Asp 090	Phe	Gln	Glu		Asn 095
His	Ile	Cys	Thr 1	Phe 100	Lys	Gln	Thr		Glu 105	Asn	Tyr	Arg		Pro 110
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<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic Oligonucleotide Probe

<400> 295

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<400> 296
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Gln Pro Arg Cys Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys
Lys Cys His Pro Gly Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu
Asn Glu Cys Gly Leu Lys Pro Arg Pro Cys Lys His Arg Cys Met
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Leu Met Pro Asp Gly Ser Cys Ser Ser Ala Leu Thr Cys Ser Met
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Cys Gln Cys Pro Ser Pro Gly Leu His Leu Ala Pro Asp Gly Arg
Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly Arg Ala Ser Cys
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Lys Cys His Lys Gly Phe Asp Leu Met Tyr Ile Gly Gly Lys Tyr
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Gln Cys His Asp Ile Asp Glu Cys Ser Leu Gly Gln Tyr Gln Cys
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His	Ser	Cys	Asn	Phe 395	Asp	His	Gly	Leu	Cys 400	Gly	Trp	Ile	Arg	Glu 405
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Ala	Ala	Arg	Leu	Val 440	Leu	Pro	Leu	Gly	Arg 445	Leu	Met	His	Ser	Gly 450
Asp	Leu	Cys	Leu	Ser 455	Phe	Arg	His	Lys	Val 460	Thr	Gly	Leu	His	Ser 465
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Ala	Leu	Trp	Gly	Arg 485	Asn	Gly	Gly	His	Gly 490	Trp	Arg	Gln	Thr	Gln 495
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Lys Pro Val Val Gln Ile His Pro Pro Ser Gly Ala Val Glu Tyr 140 145 150

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Arg Pro Glu Thr Glu Tyr Arg Lys Ala Gln Thr Phe Ser Gly His 380 385 390

Glu Asp Ala Leu Asp Asp Phe Gly Ile Tyr Glu Phe Val Ala Phe 395 400 405

Pro Asp Val Ser Gly Val Ser Arg Ile Pro Ser Arg Ser Val Pro 410 415 420

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Val Arg Val Ile Thr Asp Glu Asn Trp Arg Glu Leu Leu Glu Gly 35 40 45

Asp Trp Met Ile Glu Phe Tyr Ala Pro Trp Cys Pro Ala Cys Gln 50 55 60

Asn Leu Gln Pro Glu Trp Glu Ser Phe Ala Glu Trp Gly Glu Asp
65 70 75

Leu Glu Val Asn Ile Ala Lys Val Asp Val Thr Glu Gln Pro Gly 80 85 90

Leu Ser Gly Arg Phe Ile Ile Thr Ala Leu Pro Thr Ile Tyr His 95 100 105

Cys Lys Asp Gly Glu Phe Arg Arg Tyr Gln Gly Pro Arg Thr Lys 110 115 120

Lys Asp Phe Ile Asn Phe Ile Ser Asp Lys Glu Trp Lys Ser Ile 125 130 135

Glu Pro Val Ser Ser Trp Phe Gly Pro Gly Ser Val Leu Met Ser 140 145 150

Ser Met Ser Ala Leu Phe Gln Leu Ser Met Trp Ile Arg Thr Cys 155 160 165

His Asn Tyr Phe Ile Glu Asp Leu Gly Leu Pro Val Trp Gly Ser 170 175 180

Tyr Thr Val Phe Ala Leu Ala Thr Leu Phe Ser Gly Leu Leu Leu 185 190 195

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Ala Asp Glu Glu Asp Val Ser Glu Glu Glu Ala Glu Ser Lys Glu
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<sup>&</sup>lt;211> 533

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250

270

Glu Glu Arg Glu Lys Thr Leu Thr Asn Gln Thr Glu Ala Glu Leu

260

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Glu	Arg	Asp	Val	Tyr 290	Glu	Ser	Leu	Cys	Arg 295	Gly	Glu	Gly	Val	Lys 300
Leu	Thr	Pro	Arg	Arg 305	Gln	Lys	Arg	Leu	Phe 310	Cys	Arg	Tyr	His	His 315
Gly	Asn	Arg	Ala	Pro 320	Gln	Leu	Leu	Ile	Ala 325	Pro	Phe	Lys	Glu	Glu 330
Asp	Glu	Trp	Asp	Ser 335	Pro	His	Ile	Val	Arg 340	Tyr	Tyr	Asp	Val	Met 345
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Val	Ala	Ser	Tyr	Arg 380	Val	Ser	Lys	Ser	Ser 385	Trp	Leu	Glu	Glu	Asp 390
Asp	Asp	Pro	Val	Val 395	Ala	Arg	Val	Asn	Arg 400	Arg	Met	Gln	His	Ile 405
Thr	Gly	Leu	Thr	Val 410	Lys	Thr	Ala	Glu	Leu 415	Leu	Gln	Val	Ala	Asn 420
Tyr	Gly	Val	Gly	Gly 425	Gln	Tyr	Glu	Pro	His 430	Phe	Asp	Phe	Ser	Arg 435
Arg	Pro	Phe	Asp	Ser 440	Gly	Leu	Lys	Thr	Glu 445	Gly	Asn	Arg	Leu	Ala 450
Thr	Phe	Leu	Asn	Tyr 455	Met	Ser	Asp	Val	Glu 460	Ala	Gly	Gly	Ala	Thr 465
Val	Phe	Pro	Asp	Leu 470	Gly	Ala	Ala	Ile	Trp 475	Pro	Lys	Lys	Gly	Thr 480
Ala	Val	Phe	Trp	Tyr 485	Asn	Leu	Leu	Arg	Ser 490		Glu	Gly	Asp	Tyr 495
Arg	Thr	Arg	His	Ala 500		Cys	Pro	Val	Leu 505		Gly	Cys	Lys	Trp 510
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235

250

255

Pro His Leu Asp Gly Cys Arg Gly Asp Ile Leu Ser Ala Arg Pro

230

245

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				425	Lys				430					435
	•			440	Gly			-	445		_			450
				455	Arg				460					465
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				500	Ala				505					510
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Gly	Gly	Arg	Phe	Asp 665	Arg	Gln	Ala	Ser	Ala 670	Glu	Gly	Cys	Phe	Tyr 675
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Ala	Gly	Gln	Glu	Glu 695	Glu	Glu	Ala	Leu	Glu 700	Gly	Leu	Glu	Val	Met 705
Asp	Val	Phe	Leu	Arg 710	Phe	Ser	Gly	Leu	His 715	Leu	Phe	Arg	Ala	Val 720
Glu	Pro	Gly	Leu	Val 725	Gln	Lys	Phe	Ser	Leu 730	Arg	Asp	Cys	Ser	Pro 735
Arg	Leu	Ser	Glu	Glu 740	Leu	Tyr	His	Arg	Cys 7 <b>4</b> 5	Arg	Leu	Ser	Asn	Leu 750
Glu	Gly	Leu	Gly	Gly 755	Arg	Ala	Gln	Leu	Ala 760	Met	Ala	Leu	Phe	Glu 765
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Gly His Gly Asn Arg Met His His His Glu His His Leu Gln 35 40 45

Ala Pro Asn Lys Glu Asp Ile Leu Lys Ile Ser Glu Asp Glu Arg
50 55 60

Met Glu Leu Ser Lys Ser Phe Arg Val Tyr Cys Ile Ile Leu Val 65 70 75

Lys Pro Lys Asp Val Ser Leu Trp Ala Ala Val Lys Glu Thr Trp 80 85 90

Thr Lys His Cys Asp Lys Ala Glu Phe Phe Ser Ser Glu Asn Val95 100 105

Lys Val Phe Glu Ser Ile Asn Met Asp Thr Asn Asp Met Trp Leu 110 115 120

Met Met Arg Lys Ala Tyr Lys Tyr Ala Phe Asp Lys Tyr Arg Asp 125 130 135

Gln Tyr Asn Trp Phe Phe Leu Ala Arg Pro Thr Thr Phe Ala Ile 140 145 150

Ile Glu Asn Leu Lys Tyr Phe Leu Leu Lys Lys Asp Pro Ser Gln
155 160 165

Pro Phe Tyr Leu Gly His Thr Ile Lys Ser Gly Asp Leu Glu Tyr 170 175 180

Val Gly Met Glu Gly Gly Ile Val Leu Ser Val Glu Ser Met Lys 185 190 195

Arg Leu Asn Ser Leu Leu Asn Ile Pro Glu Lys Cys Pro Glu Gln 200 205 210

Gly Gly Met Ile Trp Lys Ile Ser Glu Asp Lys Gln Leu Ala Val 215 220 225

Cys Leu Lys Tyr Ala Gly Val Phe Ala Glu Asn Ala Glu Asp Ala

230 235 240 Asp Gly Lys Asp Val Phe Asn Thr Lys Ser Val Gly Leu Ser Ile 245 Lys Glu Ala Met Thr Tyr His Pro Asn Gln Val Val Glu Gly Cys 260 265 Cys Ser Asp Met Ala Val Thr Phe Asn Gly Leu Thr Pro Asn Gln Met His Val Met Met Tyr Gly Val Tyr Arg Leu Arg Ala Phe Gly 295 290 His Ile Phe Asn Asp Ala Leu Val Phe Leu Pro Pro Asn Gly Ser 305 Asp Asn Asp <210> 342 <211> 23 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 342 tececaagee gttetagaeg egg 23 <210> 343 <211> 18 <212> DNA <213> Artificial Sequence <223> Synthetic Oligonucleotide Probe <400> 343 ctggttcttc cttgcacg 18 <210> 344 <211> 28 <212> DNA <213> Artificial Sequence <220> <223> Synthetic Oligonucleotide Probe <400> 344 gcccaaatgc cctaaggcgg tatacccc 28 <210> 345 <211> 50 <212> DNA

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atttctcagt gcctgtttca tcaccagatg tgttgtgaca tttcgcatct 250
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gaactgggaa tattttcaat ccagctgcta cttcttttct actgacacca 400
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qtqqttatca actcacagga qgagcaggaa ttcctttcct acaagaaacc 500
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Phe Arg Ile Phe Gln Thr Cys Asp Glu Lys Lys Phe Gln Leu Pro 50 55 60												
Glu Asn Phe Thr Glu Leu Ser Cys Tyr Asn Tyr Gly Ser Gly Ser 65 70 75												
Val Lys Asn Cys Cys Pro Leu Asn Trp Glu Tyr Phe Gln Ser Ser 80 85 90												
Cys Tyr Phe Phe Ser Thr Asp Thr Ile Ser Trp Ala Leu Ser Leu 95 100 105												
Lys Asn Cys Ser Ala Met Gly Ala His Leu Val Val Ile Asn Ser 110 115 120												
Gln Glu Glu Gln Glu Phe Leu Ser Tyr Lys Lys Pro Lys Met Arg 125 130 135												
Glu Phe Phe Ile Gly Leu Ser Asp Gln Val Val Glu Gly Gln Trp 140 145 150												
Gln Trp Val Asp Gly Thr Pro Leu Thr Lys Ser Leu Ser Phe Trp 155 160 165												
Asp Val Gly Glu Pro Asn Asn Ile Ala Thr Leu Glu Asp Cys Ala 170 175 180												
Thr Met Arg Asp Ser Ser Asn Pro Arg Gln Asn Trp Asn Asp Val 185 190 195												
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<212> PRT

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